

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model.

Run on: September 5, 2004, 10:24:46 ; Search time 21 Seconds

(without alignments)
59.547 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASEIGKSTNTFC 13

Scoring table: BLOSUM62

Gapext 0.5

Searched: 283366 seqs, 961.91526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	33.5	46.5	12	2	PT0216		T-cell receptor beta chain V-J region - mouse (fragment)
2	30	41.7	12	2	S47394		T-cell receptor beta chain - mouse
3	29.5	41.0	13	2	S47357		T-cell receptor beta chain - mouse
4	29	40.3	12	2	S25549		T-cell receptor beta chain - mouse
5	28	38.9	12	2	PH1463		T-cell receptor beta chain - mouse
6	28	38.9	12	2	PH1466		T-cell receptor beta chain - mouse
7	28	38.9	13	2	S47400		T-cell receptor beta chain - mouse
8	27	37.5	11	2	PT0217		T-cell receptor beta chain - mouse
9	27	37.5	12	2	S47391		T-cell receptor beta chain - mouse
10	27	37.5	13	2	S47383		T-cell receptor beta chain - mouse
11	26	36.1	11	2	S57575		T-cell receptor beta chain - mouse
12	26	36.1	12	2	S47392		T-cell receptor beta chain - mouse
13	26	36.1	13	2	S47381		T-cell receptor beta chain - mouse
14	25.5	35.4	13	2	PH1457		T-cell receptor beta chain - mouse
15	25	34.7	10	2	S23371		T-cell receptor beta chain - mouse
16	25	34.7	11	2	PH0947		T-cell receptor beta chain - mouse
17	25	34.7	12	2	PH1469		T-cell receptor beta chain - mouse
18	25	34.7	12	2	PH0931		T-cell receptor beta chain - mouse
19	24.5	34.0	12	2	PH1451		T-cell receptor beta chain - mouse
20	24	33.3	11	2	PH1583		T-cell receptor beta chain - mouse
21	24	33.3	12	2	S26552		T-cell receptor beta chain - mouse
22	24	33.3	12	2	S26559		T-cell receptor beta chain - mouse
23	24	33.3	12	2	S26554		T-cell receptor beta chain - mouse
24	24	33.3	12	2	S47363		T-cell receptor beta chain - mouse
25	24	33.3	12	2	PH1467		T-cell receptor beta chain - mouse
26	24	33.3	12	2	PH1468		T-cell receptor beta chain - mouse
27	24	33.3	13	2	S47390		T-cell receptor beta chain - mouse
28	23.5	32.6	12	2	PH1459		T-cell receptor beta chain - mouse
29	23.5	32.6	13	2	S47377		T-cell receptor beta chain - mouse

RESULT 1
PT0216
T-cell receptor beta chain V-J region (4-1-G-4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0216

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A;Reference number: PT0209; PMID:91217621; PMID:1902501

A;Accession: PT0216

A;Molecule type: mRNA

A;Residues: 1-12 <NAK>

C;Keywords: T-cell receptor

RESULT 2
S47394
T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47369

R;Lerner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cells

A;Reference number: S47355

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-12 <IEH>

A;Cross-references: EMBL:Z35714; NID:CAA84783.1; PID:CAA84783.1; PMID:9527524; EMBL:Z35694;

C;Keywords: T-cell receptor

Query Match 41.7%; Score 30; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 51;

Matches 6; Conservativeness 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASEIGKSTNTF 12

Db 1 CASSIGNYGYTF 12

RESULT 3
S47357

ALIGNMENTS

RESULT 1
PT0216
T-cell receptor beta chain V-J region (4-1-G-4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A;Reference number: PT0209; PMID:91217621; PMID:1902501

A;Accession: PT0216

A;Molecule type: mRNA

A;Residues: 1-12 <NAK>

C;Keywords: T-cell receptor

Query Match 46.5%; Score 33.5; DB 2; Length 12;

Best Local Similarity 72.7%; Pred. No. 12;

Matches 8; Conservativeness 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CASEIGKSTNT 11

Db 1 CASSIG-TNT 10

T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47357
 R;LInnher, P.J.
 submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell receptor number: S47355
 A;Accession: S47357
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35681; NID:9527451; PIDN:CAA84750.1; PID:9527452
 C;Keywords: T-cell receptor

Query Match Score 29.5%; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 1; Gaps 1;

QY 1 CASELGK8 8
 Db 1 CASSLGNT 8

RESULT 6
 PH1466
 T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1466
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, A.; Regnault, A.; Ko J. Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatibility genes
 A;Reference number: PH1430; PMID:93171821; PMID:8436911
 A;Accession: PH1466
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>
 C;Experimental source: cytolytic T-lymphocyte
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match Score 28%; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
 Db 1 CASSLGQ 7

RESULT 7
 S47400
 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47400
 R;Lechner, P.J.
 submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell receptor number: S47355
 A;Accession: S47400
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35678; NID:9527535; PIDN:CAA84747.1; PID:9527536
 C;Keywords: T-cell receptor

Query Match Score 28%; DB 2; Length 13;
 Best Local Similarity 41.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
 Db 1 CASSVALATEAF 12

RESULT 8
 PT0217
 T-cell receptor beta chain V-J region (4-1-E-2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C;Accession: PT0217
 R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
 A;Reference number: PT0209; PMID:91217621; PMID:1902501
 A;Accession: PT0217
 A;Molecule type: mRNA

A;Residues: 1-12 <CAS>
 A;Experimental source: cytolytic T-lymphocyte
 A;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

A;Residues: 1-11 <NAK>
 C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 11;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CASELKG 6
 Db 1 CASRLIG 6

RESULT 9

S47391 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47391; S47386
 R;Lechner, P.J.
 submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47355
 A;Accession: S47331
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <LEH>
 A;Cross-references: EMBL:Z35712; NID:9527519; PIDN:CAA84781.1; PID:9527520; EMBL:Z35701;
 C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTF 12
 Db 1 CASSTGSGYTF 12

RESULT 10

S47383 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47383
 R;Lechner, P.J.
 submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47355
 A;Accession: S47383
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35709; NID:9527513; PIDN:CAA84778.1; PID:9527514
 C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CASELGKS 8
 Db 1 CASSMGGS 8

RESULT 11

S57575 T cell receptor V-J junctional alpha chain region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
 C;Accession: S57575
 R;Burrows, S.R.; Salins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
 submitted to the EMBL Data Library, June 1995
 A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b

A;Reference number: S57494
 A;Accession: S57575
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-11 <BUR>
 A;Cross-references: EMBL:Z49953; NID:9887510; PIDN:CAA90224.1; PID:9887511
 C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CASELGK 7
 Db 1 CASQGCK 7

RESULT 12

S47395 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47395
 R;Lechner, P.J.
 submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47355
 A;Accession: S47395
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <LEH>
 A;Cross-references: EMBL:Z35715; NID:9527525; PIDN:CAA84784.1; PID:9527526
 C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTF 12
 Db 1 CASSQSYGYTF 12

RESULT 13

S47381 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47381
 R;Lechner, P.J.
 submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47355
 A;Accession: S47381
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35608; NID:9527487; PIDN:CAA84767.1; PID:g527488
 C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 41.7%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTF 12
 Db 1 CASSSTRNTAEAF 12

RESULT 14

S47382 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47382; S47370
 R;Lehner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47355
 A;Accession: S47382
 A;Keywords: T-cell receptor
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35687; NID:9527463; PIDN:CAA84756.1; PID:9527464; EMBL:Z35695;

Query Match 35.4%; Score 25.5; DB 2; Length 13;
 Best Local Similarity 54.5%; Pred. No. 3.6e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 CASEFGKSTNT 11
 ||| : |||:
 Db 1 CASSM-RSTDT 10

RESULT 15
 S23371
 T-cell receptor alpha chain J region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: S23371 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Bichman
 Eur. J. Immunol. 21, 2749-2754, 1991
 A;Title: Biased T cell receptor (Valpha) region repertoire in the synovial fluid of rheu
 A;Reference number: S23364; MUID:1657615
 A;Accession: S23371
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-10 <PLU>
 A;Cross-references: EMBL:X58166
 C;Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 ASELGKST 9
 ||| : |||:
 Db 2 SGEAGKST 9

Search completed: September 5, 2004, 10:32:20
 Job time : 21 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	23	31.9	12	1	PSP3_PHYPA	P8062 phycomitri
2	20	27.8	12	1	V23K_WSSV	P82005 white spot
3	20	27.8	13	1	LIGA_TRAVE	P20011 trametes ve
4	20	27.8	13	1	PSBP_PIPNS	P81658 pinus pinas
5	19	26.4	10	1	CORM_RAT	P80431 rattus norv
6	18	25.0	12	1	UR2B_CATCO	P04559 catostomus
7	18	25.0	13	1	FARB_ASSSU	P43173 ascaris suu
8	17	23.6	12	1	UR2B_CYPCA	P04561 cyprinus ca
9	16	22.2	9	1	XYLA_STRSQ	P19149 streptomyce
10	16	22.2	11	1	TXC2_CALVO	P4518 calliphora
11	16	22.2	12	1	CXL3_CONMR	P58809 conus marmo
12	16	22.2	12	1	TA10_TREME	P01371 tremella me
13	16	22.2	13	1	CXDA_CONST	P28878 conus stria
14	16	22.2	13	1	HPB9_RANES	P32416 rana escula
15	15	20.9	9	1	CCAP_CARMA	P38556 carcinus ma
16	15	20.8	9	1	FAR5_ACSCU	P43170 ascaris suu
17	15	20.8	9	1	SAMP_MUSCA	P19095 mustelus ca
18	15	20.8	9	1	SAP_STOVA	P24047 stomopante
19	15	20.8	10	1	COK0_RABIT	P80336 oryctolagus
20	15	20.8	10	1	ODE2_BOVIN	P11180 bos taurus
21	15	20.8	11	1	CX5A_CONAL	P58848 conus aulic
22	15	20.8	11	1	CX5B_CONAL	P58849 conus aulic
23	15	20.8	11	1	FAR9_CALVO	P41864 calliphora
24	15	20.8	11	1	TINI_HOPTI	P82651 hoplobarac
25	15	20.8	12	1	CXA1_CONIN	P50983 conus imper
26	15	20.8	12	1	NO40_LOTJA	O22426 lotus japon
27	15	20.8	12	1	SOP5_BACSU	P80853 bacillus su
28	15	20.8	13	1	CRBL_VESTR	P17231 vespa tropi
29	15	20.8	13	1	CXA2_COANGE	P01520 conus geogr
30	15	20.8	13	1	GFR1_HORVU	P28525 hordeum vul
31	15	20.8	13	1	GFR2_HORVU	P28526 hordeum vul
32	14	19.4	7	1	IGAO_DACDE	P06294 dactylum d
33	14	19.4	7	1	UC24_MAIZE	P80630 zea mays (m

ALIGNMENTS						
RESULT 1						
PSP3_PHYPA	PSP3_PHYPA	STANDARD;	PRT;	12 AA.		
AC	P8062;					
DT	01-OCT-1996 (Rel. 34, Created)					
DT	01-OCT-1996 (Rel. 34, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Oxygen-evolving enhancer protein 2 (OEE2) (24 kDa subunit of oxygen evolving system of photosystem II) (Fragment).					
OS	Physcomitrella patens (Moss).					
OC	Bryopsida; Viridiplanteae; Streptophytina; Embryophytina; Bryophyta; Funariidae; Funariales; Physcomitrella.					
RN	[1]					
RP	SEQUENCE.					
RC	TISSUE-Protonema;					
RX	Medline=97275459; PubMed=9129336;					
RA	Kasten B., Buck F., Nuske J., Reski R.;					
RT	"Cytokinin effects" nuclear- and plastome-encoded energy-converting					
RT	plastid enzymes";					
RL	Planta 201:261-272 (1997).					
CC	- - FUNCTION: May be involved in the regulation of photosystem II.					
CC	- - SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex.					
CC	- - INDUCTION: By light.					
CC	- - SIMILARITY: Belongs to the psbp family.					
KW	Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane; Multigene family;					
PT	NON-TER	12	AA;	1182 MW;	8D2B01D54D7C44DC5 CRC64;	
SEQUENCE						
Qy	6 GKRSTNF 12					
	: : :					
Db	3 GESANTF 9					
RESULT 2						
V23K_WSSV	V23K_WSSV	STANDARD;	PRT;	12 AA.		
ID	V23K_WSSV					
AC	P8205;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DB	23 kDa structural polyprotein (Fragment).					
OS	White spot syndrome virus (WSSV).					
OC	Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whipovirus.					
OX	RNA TaxID=92652;					
RN	[1] SEQUENCE.					
RC	STRAN-South Carolina;					
RX	Medline=20214117; PubMed=10752552;					
RA	Wang Q., Poulios B.T., Lightner D.V.;					

"Protein analysis of geographic isolates of shrimp white spot syndrome virus";
 RT Arch. Virol. 145: 263-274 (2000).
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 FT NON TER 12 12
 SEQUENCE 12 AA; 1323 MW;
 OCOP41E91D51A724 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 12;
 Best Local Similarity 57.1%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ELGKSTN 10
 Db 2 EFGNUTN 8

RESULT 3
 LIGA_TRAVE STANDARD PRT; 13 AA.
 ID LIGA_TRAVE
 AC P2011;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 24-FEB-2003 (Rel. 41, Last annotation update)
 DS Ligninase A (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin peroxidase) (Fragment).
 OS Trametes versicolor (White-rot fungus).
 OC Bacterio; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphylophorales; Trametes.
 OC NCBI_TaxID=5325;
 RN [1]

RP
 SEQUENCE:
 MEDLINE=9211432; PubMed=2707445;
 RA Joessson L, Karlsson O, Jandquist K, Nyman P.O.;
 RT "Trametes versicolor ligninase: Isozyme sequence homology and substrate specificity";
 RL FEBS Lett. 247:143-146 (1989).
 CC -!- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-C(beta) cleavage of the propyl side chains of lignin.
 CC -!- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,3-diol + H(2)O(2) = veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol + 4 H(2)O.
 CC -!- PATHWAY: Lignin degradation; first step.
 CC -!- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
 DR PIR; S04013; S04016; Peroxidase.
 DR PROSITE; PS00435; PEROXIDASE_1; PARTIAL.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
 KW Multigene family; Lignin degradation.
 SQ SEQUENCE 13 AA; 1298 MW; 22C50BD5872A4338 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GKSTNT 11
 Db 6 GRNTAT 11

RESULT 4
 PSBP_PINPS STANDARD PRT; 13 AA.
 ID PSBP_PINPS
 AC P81658;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Oxygen-evolving enhancer Protein 2 (OEE2) (23 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
 DE PSBP.
 GS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;

UR2B_CATCO		STANDARD;	PRT;	12 AA.
ID P04559;				
DT 13-AUG-1987 (Rel. 05, Created)				
DT 13-AUG-1987 (Rel. 05, Last sequence update)				
DT 10-OCT-2003 (Rel. 42, Last annotation update)				
DE Urotselin IIB (U-IIIB) (UIIIB). Catostomidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes; Catostomidae; Catostomus.				
OC				
OC				
OX NCBI_TaxID=7971;				
RN [1]				
RP SEQUENCE:				
RX MEDLINE=84041959; PubMed=6138758;				
RA McMaster D., Lederis K.;				
RT "Isolation and amino acid sequence of two urotselin II peptides from Catostomus commersoni urophyses.";				
RL Peptides 4:367-373 (1983)				
CC -!- FUNCTION: Urotselin is found in the teleost caudal neurosecretory system. It has a suggested role in osmoregulation and as a corticotropin-releasing factor.				
CC -!- SUBCELLULAR LOCATION: Secreted.				
CC -!- SIMILARITY: Belongs to the urotselin 2 family.				
DR PIR: JS0424; JS0424.				
DR InterPro: IPR0143; Urotselin_II.				
DR Pfam: PF02083; Urotselin_II; 1.				
KW Hormone.				
FT DISULFID 6 11				
FT DISULFID 6 11				
SQ SEQUENCE 12 AA; 1437 MW; 73961BDBB879CEBB CRC64;				
Query Match 25.0%; Score 18; DB 1; Length 12;				
Best Local Similarity 60.0%; Pred. No. 2.7e+03;				
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
Qy 9 TNTFC 13				
Db 2 SNTFC 6				
RESULT 7				
FARB_ASCSU		STANDARD;	PRT;	13 AA.
ID FARB_ASCSU				
AC P43173;				
DT 01-NOV-1995 (Rel. 32, Created)				
DT 01-NOV-1995 (Rel. 32, Last sequence update)				
DT 01-FEB-1996 (Rel. 33, Last annotation update)				
DB FMRFamide-like neuropeptide AF11.				
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).				
OC Eukaryota; Metazoa; Nematoidea; Ascaridida; Ascaridoidea; Nematoda; Chromadora; Ascaridida; Ascaris.				
OC				
OX NCBI_TaxID=6253;				
RN [1]				
RP SEQUENCE:				
RX MEDLINE=953380362; PubMed=7651904;				
RA Cowden C., Stretton A.O.W.;				
RT Eight novel FMRFamide-like neuropeptides isolated from the nematode Ascaris suum.;				
RL Peptides 16:491-500(1995).				
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.				
CC Neuropeptide; Amidation.				
KW MOD RES 13 13				
FT AMIDATION.				
SQ SEQUENCE 13 AA; 1495 MW;				
Query Match 25.0%; Score 18; DB 1; Length 13;				
Best Local Similarity 40.0%; Pred. No. 2.9e+03;				
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;				
Qy 3 SELGKSTNTF 12				
Db 1 SDIGISEPNF 10				

DR	PROSITE; PS00173; XYLOSE ISOMERASE 2; PARTIAL.	RT	venom of <i>Coranus marmoreus</i> .";	
KW	Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.	RL	J. Biol. Chem. 275:3916-39522 (2000).	
FT	9 g	CC	-1; FUNCTION: Inhibits the neuronal noradrenaline transporter.	
SQ	SEQUENCE 9 AA; 983 MW; F64BA1EDC5B87DD1 CRC64;	CC	-1; SUBCELLULAR LOCATION: Secreted.	
		CC	-1; TISSUE SPECIFICITY: Expressed by the venom duct.	
		CC	-1; MASS SPECTROMETRY: MW=1262.77; MW ERA=0.07; METHOD=D-Electrospray.	
		CC	-1; SIMILARITY: Belongs to the chi/lambda-conotoxin family.	
		KW	Neurotoxin; Toxin; Hydroxylation.	
		FT	DISULFID 3 12	
		FT	DISULFID 4 9	
		FT	MOD RES 11 11 HYDROXYLATION.	
		SQ	SEQUENCE 12 AA; 1251 MW; 277AAE2422D5A2C8 CRC64;	
Qy	8 STNTNF 12	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
Db	5 SAHTP 9	Best Local Similarity 60.0%; Pred. No. 1.e+05; Indels 0; Gaps 0;	Pred. No. 6.2e+03; Indels 0; Gaps 0;	
RESULT 10	TRC2_CALVO	STANDARD; PRT; 11 AA.	Best Local Similarity 66.7%; Pred. No. 6.2e+03; Length 12;	
ID	TRC2_CALVO	STANDARD; PRT; 11 AA.	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
AC	P41518;	Qy 11 NTFC 13	Score 16; DB 1; Length 12;	
DT	01-NOV-1995 (Rel. 32, Created)	Db 7 SF9 9	Pred. No. 6.2e+03; Length 12;	
DR	10-OCT-2003 (Rel. 32, Last sequence update)	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
DE	10-OCT-2003 (Rel. 42, Last annotation update)	Best Local Similarity 66.7%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
OS	Callitachynkin II.	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Qy 11 NTFC 13	Score 16; DB 1; Length 12;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;	Db 7 SF9 9	Pred. No. 6.2e+03; Length 12;	
OC	Calliphoridae; Calliphora.	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
OX	NCBI_TAXID=27454;	Best Local Similarity 66.7%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RN	[1]	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RP	AND SYNTHESIS.	Qy 11 NTFC 13	Score 16; DB 1; Length 12;	
RX	SEQUENCE=95-075727; PubMed=7984492;	Db 7 SF9 9	Pred. No. 6.2e+03; Length 12;	
RA	Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RA	Nassei D.R.;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RA	"Callitachynkin I and II, two novel myotropic peptides isolated from the blowfly, Calliphora vomitoria, that have resemblances to tachykinins";	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	Peptides 15:761-768 (1994)	Qy 11 NTFC 13	Score 16; DB 1; Length 12;	
RT	-1; FUNCTION: Myoactive peptide.	Db 7 SF9 9	Pred. No. 6.2e+03; Length 12;	
CC	-1; SUBCELLULAR LOCATION: Secreted.	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
CC	-1; SIMILARITY: SOME SIMILARITY TO TACHYKININS.	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
KW	Tachykinin; Neuropeptide; Amidation.	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
MOD RES	11 11 15DTEB39C5CDD444 CRC64;	Qy 11 NTFC 13	Score 16; DB 1; Length 12;	
SQ	SEQUENCE 11 AA; 1103 MW; 15DTEB39C5CDD444 CRC64;	Db 7 SF9 9	Pred. No. 6.2e+03; Length 12;	
Query Match Score 16; DB 1; Length 11;	Query Match Score 16; DB 1; Length 12;	Query Match Score 16; DB 1; Length 12;	Query Match Score 16; DB 1; Length 12;	
Best Local Similarity 42.9%; Pred. No. 5.7e+03; Length 11;	Best Local Similarity 42.9%; Pred. No. 5.7e+03; Length 11;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 1; Indels 1; Gaps 0;	Matches 2; Conservative 1; Mismatches 1; Indels 1; Gaps 0;	
Qy 6 GKSTNTNF 12	FT LIPID 12	FT LIPID 12	FT LIPID 12	
Db 1 GLGNNAF 7	MOD RES 12	MOD RES 12	MOD RES 12	
	SEQUENCE 12 AA; 12446 MW; 84EE574959676DC5 CRC64;	SEQUENCE 12 AA; 12446 MW; 84EE574959676DC5 CRC64;	SEQUENCE 12 AA; 12446 MW; 84EE574959676DC5 CRC64;	
RESULT 11	CXL3_CONNR	STANDARD; PRT; 12 AA.	Qy 10 NTFC 13	Score 16; DB 1; Length 12;
ID	CXL3_CONNR	STANDARD; PRT; 12 AA.	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;
AC	P58809;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
DT	28-FEB-2003 (Rel. 41, Created)	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
DE	Lambda-conotoxin CMX.	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
OS	Conus marmoreus (Marble cone).	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
OC	Eukaryota; Metazoa; Mollusca; Gastrooda; Orthogastropoda; Neogastropoda; Conoidea; Conidae; Conus.	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
OX	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H., "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RX	20564325; PubMed=10983292;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H., "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RA	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
RT	RT TISSUE=Venom;	Qy 10 NTFC 13	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Db 9 NGYC 12	Pred. No. 6.2e+03; Length 12;	
RT	RT TISSUE=Venom;	Query Match Score 16; DB 1; Length 12;	Score 16; DB 1; Length 12;	
RT	RT TISSUE=Venom;	Best Local Similarity 50.0%; Pred. No. 6.2e+03; Length 12;	P	

RESULT 14
HPB9_RANES
 ID HPB9_RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-2003 (Rel. 42, Last annotation update)
 DE Hemolytic protein B9 (Fragment).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 RN [1]
 RP
 SEQUENCE:
 TISSUE-SKIN secretion;
 MEDLINE=9019865; PubMed=2317508;
 RA Simmaco M.; de Biase D.; Severini C.; Aita M.; Erspermer G.F.;
 Barra D.; Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 extracts of Rana esculenta."
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -!- FUNCTION: Shows hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S09019; S09019.
 KW Amphibian defense peptide; Amidation; Hemolysis.
 FT MOD RES 13 13 AMIDATION.
 FT NON_TER 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457BBD CRC64;
 Query Match Score 16; DB 1; Length 13;
 Best Local Similarity 37.5%; Pred. No. 6.7e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CASELGK 8
 Db 3 CHFACGRN 10

RESULT 15
CCAP_CARMA
 ID CCAP_CARMA STANDARD; PRT; 9 AA.
 AC P38556;

DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cardioactive Peptide (CCAP).
 OS Carcinus maenas (Common shore crab) (Green crab),
 Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
 Tenbrio molitor (Yellow mealworm), and
 Spodoptera eridania (Southern armyworm).
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Bivalacocetacea; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC EuBrachyura; Portunoidea; Portunidae; Carcinus.
 NCBI_TaxID=6759, 7130, 7067, 37547;
 RN [1]
 RP
 SEQUENCE:
 SPECIES=C.magna; TISSUE=Pericardial organs;
 RC "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 shore crab *Carcinus magna*";
 RA Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
 RN [2]
 RP
 SEQUENCE:
 SPECIES=M.sexta; TISSUE=Pericardial organs;
 RX MEDLINE=93050243; PubMed=1426284;
 RA Furuya K., Hilbich C., Beyreuther K., Keller R.;
 Cheung C.C., Loi P.K., Syvester A.W., Lee T.D., Tublitz N.J.;
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 hawkmoth, *Manduca sexta*."
 RL FBPS Lett. 313:165-168(1992).
 RN [3]
 RP
 SEQUENCE:
 SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RX MEDLINE=94176032; PubMed=8129851;
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
 Schooler D.A.,
 RT "Isolation and identification of a cardioactive peptide from *Tenbrio*
 molitor and *Spodoptera eridania*";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
 CC -!- FUNCTION: The effect of CCAP is both ino- and chronotropic.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Stored in pericardial organs and released
 into the hemolymph.
 DR PIR; A26363; A26363.
 DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.
 FT DISURID 3 9 AMIDATION.
 FT MOD RES 3 9 AMIDATION.
 SQ SEQUENCE 9 AA; 959 MW; C5A861ACDD44EB9 CRC64;
 Query Match Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 2; Conservative 0; Mismatches 0; Index 0;
 Gaps 0;
 Qy 12 FC 13
 Db 2 FC 3

Search completed: September 5, 2004, 10:30:49
 Job time : 16 secs

This Page Blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW mode.

Run on: September 5, 2004, 10:22:06 ; Search time 57 Seconds
(without alignments)

71.960 Million cell updates/sec
Title: US-09-761-636A-5
Perfect score: 72

Sequence: 1 CASELGIKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL25:
 1: sp_archea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mbhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_tvirus:
 16: sp_bacteriap:
 17: sp_archaeap:
 18: sp_archeap:
 19: sp_bacteria:
 20: sp_fungi:
 21: sp_human:
 22: sp_invertebrate:
 23: sp_mbhc:
 24: sp_mammal:
 25: sp_organelle:
 26: sp_phage:
 27: sp_plant:
 28: sp_rabbit:
 29: sp_virus:
 30: sp_vertebrate:
 31: sp_tvirus:
 32: sp_bacteriap:
 33: sp_archeap:
 34: sp_archeap:
 35: sp_archeap:
 36: sp_archeap:
 37: sp_archeap:
 38: sp_archeap:
 39: sp_archeap:
 40: sp_archeap:
 41: sp_archeap:
 42: sp_archeap:
 43: sp_archeap:
 44: sp_archeap:
 45: sp_archeap:

ALIGNMENTS

RESULT 1	Q8QGZ5	PRELIMINARY;	PRT;	13 AA.
ID	Q8QGZ5;			
AC				
DT	01-JUN-2002 (TREMBLrel. 21; Created)			
DT	01-JUN-2002 (TREMBLrel. 21; Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)			
DE	Guanine nucleotide binding protein (Fragment).			
GN				
GNACO				
OS	Fugu rubripes (Japanese pufferfish). (Takifugu rubripes).			
OC	Eukaryota; Metazoa; Chorozoa; Craniata; Teleostomi; Actinopterygii; Neopterygii; Teleotei; Buteleostei; Neoteleosteis; Osteichthyes; Tetrapoda; Tetrapodidae; Takifugu.			
OC				
OC				
NCBI_TaxID=31033;				
RN	[1] _			
RP	SEQUENCE FROM N.A.			
RX	Medline=97129408; PubMed=8973916;			
RT	"G protein alpha subunit multigene family in the Japanese puffer fish genome." (Created)			
RT	"G protein alpha subunit multigene family in the Japanese puffer fish genome." (Last sequence update)			
RT	"G protein coupled receptor protein signalin. . . IEA."			
RT	Fugu rubripes: PCR From a compact vertebrate genome."			
RL	Genome Res. 6:1207-1215(1996).			
DR	EMBL: L179891; RAI77640; 1.			
DR	GO: GO:0004871; F:Signal transducer activity; IEA.			
DR	GO: GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.			
DR	"G protein alpha subunit multigene family in the Japanese puffer fish genome." (Last annotation update)			
DR	InterPro: IPR001019; Gprotein_alpha.			
DR	Pfam: PF00503; G-alpha; 1.			
FT	NON_TER	1		
FT	NON_TER	1		
SQ	SEQUENCE 13 AA; 1336 MW; 46559640B4B5B3 CRC64;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	37.5	13	Q8QGZ5	Q8QGZ5 fugu rubrip
2	26	36.1	13	Q918T4	Q918T4 human Papil
3	26	36.1	13	Q918T6	Q918T6 human Papil
4	23	31.9	12	Q9PS67	Q9PS67 gallus gall
5	21	29.2	12	Q85666	Q85666 reovirus (t
6	21	29.2	13	Q9GJU2	Q9GJU2 ovis aries
7	21	29.2	13	P82821	P82821 rana catesbe
8	21	29.2	13	P82822	P82822 rana catesbe
9	20	27.8	11	Q9T0L9	Q9T0L9 brassica ol
10	20	27.8	12	Q9R22	Q9R22 cryptococcu
11	20	27.8	12	P82820	P82820 rana catesbe
12	20	27.8	13	Q80WZ0	Q80WZ0 rattus sp.
13	20	27.8	13	P82823	P82823 rana catesbe
14	19	26.4	12	Q61331	Q61331 mus musculu
15	19	26.4	13	Q54809	Q54809 mus musculu
16	18	25.0	8	Q95213	Q95213 oryctolagus

Query Match 37.5%; Score 27; DB 13; Length 13;
Best Local Similarity 75.0%; Pred. No. 3..6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASELGSKT 9
| | | | |
1 AGESKSST 8

Dy

DE Calpastatin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Bovidae; Caprinae; Cetartiodactyla; Pecora; Bovoidea;
NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Nonneman D., Geesink G.H., Koohmaraie M.;
RT "Differential splicing and protein isoforms of ovine calpastatin.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF192534; AUG31688.1;
DR EMBL; AF192535; AUG31687.1;
FT NON TER 1
SEQUENCE 13 AA; 1335 MW; 47E9542C656BADD3 CRC64;
SQ Query Match 29.2%; Score 21; DB 6; Length 13;
Best Local Similarity 80.0%; Pred. No. 5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 GKSTN 10
Db 9 GKSTS 13

RESULT 7
P82821 PRELIMINARY;
ID P82821; PRT; 13 AA.
AC P82821; PRELIMINARY;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE RANATURINA 6
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP SEQUENCE;
RC TISSUE-SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT Ranaturins: antimicrobial peptides isolated from the skin of the
American bullfrog, *Rana catesbeiana*";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998)
CC "-; FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P:xenobiotic metabolism; IEA.
KW Antibiotic.
SQ Sequence 13 AA; 1398 MW; C85480BD0CF885BD CRC64;
Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ASELGK 7
Db 6 ASMLGK 11

RESULT 8
P82822 PRELIMINARY;
ID P82822; PRT; 13 AA.
AC P82822; PRELIMINARY;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE RANATURINA 7
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;

RN [1]
RP SEQUENCE;
RC TISSUE-SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
American bullfrog, *Rana catesbeiana*."
RL Biochem. Biophys. Res. Commun. 250:589-592(1998)
CC "-; FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P:xenobiotic metabolism; IEA.
KW Antibiotic.
SQ Sequence 13 AA; 1398 MW; C85480BD0CF885BD CRC64;
Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ASELGK 7
Db 6 ASMLGK 11

RESULT 9
Q9T0L9 PRELIMINARY;
ID Q9T0L9; PRT; 11 AA.
AC Q9T0L9; PRELIMINARY;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN SLG5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytina; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Cabrilac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaude T., Cock J.M.;
RT "The S15 self-incompatibility haplotype in *Brassica* includes three S
gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986(1999).
DR EMBL; Y18256; CAB41875.1; -.
FT NON_TER 1
SQ Sequence 11 AA; 1035 MW; CD3805DDAB772AAD CRC64;
Query Match 27.8%; Score 20; DB 10; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ASELGK 9
Db 3 ADLGCT 10

RESULT 10
Q9UR22 PRELIMINARY;
ID Q9UR22; PRT; 12 AA.
AC Q9UR22; PRELIMINARY;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STE12 alpha (Fragment).
GN STE12 ALPHA.
OS Cryptococcus neoformans var. neoformans.
OC Bacteria; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=40410;
RN [1]

RP	SEQUENCE FROM N.A.	RA	Herve D.; Rogard M.; Levi-Strauss M.;
RC	STRAIN=CBS884, BSL 3, and CBS6989;	RT	"Molecular analysis of the multiple Golf alpha subunit mRNAs in the rat brain,"
RX	MEDLINE=99380307; Pubmed=1049476;	RT	Brain Res. Mol. Brain Res. 32:125-134 (1995).
RA	Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,	RL	Brain Res. Mol. Brain Res. 32:125-134 (1995).
RA	Carter D.A.;	DR	EMBL; SB0330; AAP3222.1; -.
RT	"presence of alpha and a mating types in environmental and clinical collections of <i>Cryptococcus</i> neoformans var. gattii strains from Australia."	FT	NON_TER 13 13
RT	RL	SEQUENCE 13 AA; 1312 MW; OB6E3319671CA5B4 CRC64;	
RT	EMBL; AF155319; AAF20374.1; -.	QY	Query Match 27.8%; Score 20; DB 11; Length 13;
DR	EMBL; AF155347; AAF20372.1; -.	DR	Best Local Similarity 57.1%; Pred. No. 7.7e+03; 2; Indels 0; Gaps 0;
DR	EMBL; AF155348; AAF20373.1; -.	DB	Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
FT	NON_TER 1 1	QY	5 LGKSTNT 11
FT	NON_TER 12 12	DB	4 LGNSSKT 10
SQ	SEQUENCE 12 AA; 1307 MW; SA9DB485D5A735B7 CRC64;	RESULT 13	
QY	Query Match 27.8%; Score 20; DB 3; Length 12;	P82823	PRELIMINARY; PRT; 13 AA.
DB	Best Local Similarity 100.0%; Pred. No. 7.1e+03; 0; Indels 0; Gaps 0;	ID	P82823
QY	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	P82823; PRELIMINARY; PRT; 13 AA.
DB	11 TFC 13	DT	01-MAR-2001 (TREMBLrel. 16, Created)
QY	8 TFC 10	DR	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DB	8 TFC 10	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
RESULT 11		DE	RANATUERIN 8
ID	P82820 PRELIMINARY; PRT; 12 AA.	OS	Rana catesbeiana (Bull frog).
AC	P82820; PRELIMINARY; PRT; 12 AA.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
DT	01-MAR-2001 (TREMBLrel. 16, Created)	NCBI_TAXID	8400;
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	RN	[1]
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	RP	SEQUENCE,
DB	RANATUERIN 5.	TISSUE	=SKIN;
OS	Rana catesbeiana (Bull frog).	RX	Goraya J.; Koop F.C.; Conlon J.M.;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.	RT	"Ranatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, <i>Rana catesbeiana</i> ."
NCBI_TAXID	8400;	RT	American bullfrog. Rana catesbeiana.
RN	[1]	RL	Biochem. Biophys. Res. Commun. 250:589-592 (1998).
RP	SEQUENCE,	CC	-!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM S.AUREBUS.
RC	TISSUE=SKIN;	CC	-!- SUBCELLULAR LOCATION: SECRETED.
RX	MEDLINE=38422096; PubMed=9751476;	DR	GO; GO:0006805; P: xenobiotic metabolism; IEA.
RA	Goraya J.; Koop F.C.; Conlon J.M.;	KW	Antibiotic.
RT	"Ranatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, <i>Rana catesbeiana</i> ."	SQ	SEQUENCE 13 AA; 1414 MW; C85480BD0CF7D55D CRC64;
RT	Biochem. Biophys. Res. Commun. 250:589-592 (1998).	QY	Query Match 27.8%; Score 20; DB 13; Length 13;
CC	-!- SUBCELLULAR LOCATION: SECRETED.	DR	Best Local Similarity 83.3%; Pred. No. 7.7e+03; 0; Mismatches 1; Indels 0; Gaps 0;
CC	SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;	DB	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2 ASELGK 7	QY	2 ASELGK 7
DB	5 ASLLGK 10	DB	6 ASFLGK 11
RESULT 14		RESULT 14	
Q61331	PRELIMINARY; PRT; 12 AA.	Q61331	PRELIMINARY; PRT; 12 AA.
ID	Q61331; PRELIMINARY; PRT; 12 AA.	ID	Q61331; PRELIMINARY; PRT; 12 AA.
AC	Q61331; PRELIMINARY; PRT; 12 AA.	AC	Q61331; PRELIMINARY; PRT; 12 AA.
DT	01-NOV-1995 (TREMBLrel. 01, Created)	DT	01-NOV-1995 (TREMBLrel. 01, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	N-acetylglucosamine (Beta-1-4) Galactosyl transferase (EC 2.4.1.90)	DE	N-acetylglucosamine (Beta-1-4) Galactosyl transferase (EC 2.4.1.90)
OS	(Fragment).	OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
NCBI_TAXID	10090;	NCBI_TAXID	10090;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=8933997; PubMed=3141392;	RX	MEDLINE=8933997; PubMed=3141392;
RA	Nakazawa K.; Ando T.; Kimura T.; Narimatsu H.;	RA	Nakazawa K.; Ando T.; Kimura T.; Narimatsu H.;
RT	"Cloning and sequencing of a full-length cDNA of mouse N-	RT	"Cloning and sequencing of a full-length cDNA of mouse N-
RT	acetylglucosamine (beta1-4)galactosyltransferase."	RT	acetylglucosamine (beta1-4)galactosyltransferase."
RL	J. Biochem. 104:165-168 (1988).	RL	J. Biochem. 104:165-168 (1988).

DR EMBL; D00315; BAA00217.1; -
 DR GO; GO:0003945; FN-acetylglucosamine synthase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl...; IEA.
 KW Glycosyltransferase; Transferase activity.
 FT NON-TER 1
 FT 1
 SQ SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;
 Query Match 26.4%; Score 19; DB 11; Length 12;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ASELGKS 8
 :|||:
 Db 3 SSGGIGKT 9

RESULT 15
 OS4809 PRELIMINARY; PRT;
 ID 054809 PRELIMINARY; PRT;
 AC 054809; 13 AA.
 DT 01-JUN-1998 (TRNMBrel. 06, Created)
 DT 01-JUN-1998 (TRNMBrel. 06, Last sequence update)
 DT 01-DEC-2001 (TRNMBrel. 19, Last annotation update)
 DE Prolactin (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harigaya, T.; Imai, H.;
 RT "Partial nucleotide sequence of mouse prolactin gene, intron2.";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AB011669; BAA23091.1;
 FT NON-TER 1
 FT 1
 SQ SEQUENCE 13 AA; 1441 MW; 0B043B50DD1545B4 CRC64;
 Query Match 26.4%; Score 19; DB 11; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 8 STNTFC 13
 :|||:
 Db 7 SINSMC 12

Search completed: September 5, 2004, 10:31:54
 Job time : 59 secs

This Page Blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	ADA23476 Alzheimer
OM protein - protein search, using sw mode.		Aab26567 Human IgE
Run on:	September 5, 2004, 10:01:10 (without alignment)	Aau16900 Peptide #
Title:	US-09-761-636A-5	Abj00485 Human IgE
Perfect score:	72	Abj04090 Immunoglo
Sequence:	1 CASB1GKSTNTFC 13	Abj04092 Immunoglo
Scoring table:	BLOSUM62	Abj04093 Immunoglo
	Gapext 0.0 , Gapext 0.5	Aau08458 Peptide C
Searched:	1586107 seqs, 282547505 residues	Aav83264 NPF motif
Total number of hits satisfying chosen parameters:	383904	Aav67159 aPL immun
Minimum DB seq length: 0		Aav97980 Human syn
Maximum DB seq length: 13		Aay76718 SCP-1 HLA
Post-processing: Maximum Match 0% Listing first 45 summaries		Abp74688 Human SCP
Database :	A_Geneseq_29Jan04:*	Adc09547 Epitope w
	1: geneseqp1980s:*	Aag84316 Arabidops
	2: geneseqp1930s:*	Aag96997 Human com
	3: geneseqp2000s:*	Aag96549 Human com
	4: geneseqp2001s:*	Abp74552 N. mening
	5: geneseqp2002s:*	Abp74689 Human SCP
	6: geneseqp2003as:*	Adc09548 Epitope w
	7: geneseqp2003bs:*	
	8: geneseqp2004s:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
		ALIGNMENTS
		RESULT 1
		ID AAU04524 standard; peptide: 13 AA.
		XX
		AC AAU04524;
		XX
		DT 26-SEP-2001 (first entry)
		XX
		DE VEGF based monocyclic peptide 1.
		XX
		Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumor; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
		XX
		KW Synthetic.
		XX
		Key Location/Qualifiers
		1 : 13 /note= "This bond cyclises the peptide"
		XX
		FT Disulfide-bond
		XX
		FT FT
		XX
		PN WO200152875-A1.
		XX
		PD 26-JUL-2001.
		XX
		PF 18-JAN-2001; 2001WO-US001533.
		XX
		PR 18-JAN-2000; 2000US-0176293P.
		PR 16-MAY-2000; 2000US-0204590P.
		XX
		(LUDWIG INST CANCER RES.
		XX
		PI Achen MG, Hughes RA, Stacker S, Cendron A;
		XX
		DR WPI; 2001-442248-4/7.
		XX
		PT Novel, monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
		XX
		PT
		PT
		PT
		XX
		PS Claim 49; Page 32; 102pp; English.
		XX
		CC The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human
		CC VEGF (vascular endothelial growth factor). The invention relates to a
		CC method of producing a monomeric monocyclic peptide by a measuring beta-
		CC beta carbon separation on opposite antiparallel strands of a

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis. The condition is diabetics retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 13 AA:

Query	Match	Score 72;	DB 4;	Length 13;
	Best Local Similarity	100.0%	Pred. No. 2.1e-05;	
	Matches	13;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

DB VEGF based monocyclic peptide 12.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
XX Key Location/Qualifiers
FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX PD 26-JUL-2001.
XX PF 18-JAN-2001; 2001WO-US001533.
XX PA (LUDWIG INST CANCER RES.
XX PR 18-JAN-2000; 2000US-017623P.
PR 16-MAY-2000; 2000US-020450P.
XX DR 2001-442244/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

PT Example 25; Page 47; 102pp; English.

XX PT residues.

XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides), and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetics malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity and lymphatic vasculature. The monomeric and bicyclic peptides are used to image blood vessels and lymphatic vessels or brain. The peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

XX Sequence 13 AA:

Query Match Score 69; DB 4; Length 13;
Best Local Similarity 92.3%; Pred. No. 6.8e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CATELGKSTNTFC 13

RESULT 3
AAU04535
ID AAU04535 standard; peptide; 13 AA.
XX AC AAU04534;
XX DT 26-SEP-2001 (first entry)
XX DB VEGF based monocyclic peptide 13.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX OS Synthetic.
XX Key Location/Qualifiers
FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX PN WO200152875-A1.
XX FT 1..13 /note= "This bond cyclises the peptide"
XX PD 26-JUL-2001.
XX PR 18-JAN-2000; 2000US-017623P.
PR 16-MAY-2000; 2000US-020450P.
XX DR 2001-442244/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

PT Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides), and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetics malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity and lymphatic vasculature. The monomeric and bicyclic peptides are used to image blood vessels and lymphatic vessels or brain. The peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

XX Sequence 13 AA:

Query Match Score 69; DB 4; Length 13;
Best Local Similarity 92.3%; Pred. No. 6.8e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CATELGKSTNTFC 13

RESULT 3
AAU04535
ID AAU04535 standard; peptide; 13 AA.
XX AC AAU04535;
XX DT 26-SEP-2001 (first entry)
XX DB VEGF based monocyclic peptide 13.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX OS Synthetic.
XX Key Location/Qualifiers
FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX PN WO200152875-A1.
XX FT 1..13 /note= "This bond cyclises the peptide"
XX PD 26-JUL-2001.
XX PR 18-JAN-2000; 2000US-017623P.
PR 16-MAY-2000; 2000US-020450P.
XX DR 2001-442244/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

PA	(LUDW-) LUDWIG INST CANCER RES.	PN	WO200152875-A1.
XX	Achen MG, Hughes RA, Stacker S, Cendron A;	XX	
PI		XX	26-JUL-2001.
XX	DR WPI; 2001-442248/47.	XX	18-JAN-2001; 2001WO-US001533.
PT	Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.	CC	VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.
PT		CC	The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.
PT		CC	Sequence 13 AA;
XX	PS Example 25; Page 47; 102pp; English.	CC	Query Match 4 AAU04537 ID AAU04536 Best Local Similarity 90.3%; Score 65; DB 4; Length 13; Matches 11; Pred. No. 0.00033; Mismatches 2; Gaps 0; Indels 0; Del 0; Gaps 0; AC AAU04537; XX DT 26-SEP-2001 (first entry)
PS		CC	RESULT 4 AAU04537 ID AAU04536 standard; peptide; 13 AA.
XX		AC AAU04537; XX DT 26-SEP-2001 (first entry)	RESULT 5 AAU04536 ID AAU04536 standard; peptide; 13 AA.
XX		AC AAU04536; XX DT 26-SEP-2001 (first entry)	AAU04536
DE	VEGF based monocyclic peptide 15.	XX	DE VEGF based monocyclic peptide 14.
XX	Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.	XX	KW Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;
OS	Synthetic.	XX	KW
XX	Key Disulfide-bond Location/Qualifiers 1..13 /note= "This bond cyclises the peptide"	XX	
PH		XX	
FT		XX	
XX		XX	

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 XX Location/Qualifiers
 Key Disulfide-bond 1..13
 /note= "This bond cyclises the peptide"
 PR WO200152875-A1.
 XX 26-JUL-2001.
 PD XX
 PP 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-01762293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stackler S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX Novel monomeric monocyclic Peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
 PT Example 25; Page 47; 102pp; English.
 PS XX
 XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascular malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vessels. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
 XX Sequence 13 AA;
 SQ Query Match 84.7%; Score 61; DB 4; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.001; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CASELGSTNTFC 13
 1 :| :||| :|:
 1 CRSDVGKSTNTWC 13
 Db

XX AC AAY57039;
 XX DT 21-FEB-2000 (first entry)
 XX DE Feline immunodeficiency virus env precursor peptide #2.
 XX Feline immunodeficiency virus env precursor peptide #2.
 KW Feline immunodeficiency virus; FIV; infection; diagnosis; gp130; p55; immunogenic fragment; antibody; env precursor; gag precursor; cat; antibody binding composition.
 XX Feline immunodeficiency virus.
 XX EP962774-A1.
 XX PR 08-DEC-1999.
 XX PF 14-MAY-1999; 99EP-00303760.
 XX PR 15-MAY-1998; 98US-0065615P.
 XX PR 03-JUN-1998; 98US-00089878.
 XX (IDEXX) IDEXX LAB INC.
 PA Great RG, Mermer B, O'connor TP.
 PI XX
 DR WPI; 2000-025671/03.
 PT Diagnosing Feline Immunodeficiency Virus infection.
 XX
 PS Claim 6; Page 9; 15pp; English.
 XX This sequence is a fragment of feline immunodeficiency virus (FIV) glycoprotein 130. Peptides AAY57038-Y57039 are used in the invention as capture polypeptides when diagnosing FIV infection. The invention relates to an antibody binding composition which consists of an enhanced capture polypeptide, which contains an immunogenic fragment of FIV gag precursor p55, and a second fragment which is part of the env precursor gp130, and an antibody-binding detection composition. The invention also includes a device for performing an assay which determines whether a feline is infected with FIV. The novel method is used for the diagnosis of Feline Immunodeficiency Virus infection
 XX Sequence 12 AA;
 SQ Query Match 44.4%; Score 32; DB 3; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 ELGKSTNTFC 13
 ||| :|:
 Db 2 ELGCNQNQFC 11
 RESULT 7
 ABJ04094
 ID ABJ04094 standard; peptide; 13 AA.
 AC XX
 AC ABJ04094;
 XX DT 01-OCT-2002 (first entry)
 XX DB Immunoglobulin binding peptide #14.
 XX KW Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic; neuroprotective.
 XX OS Synthetic.
 XX PN WO200238592-A2.
 XX PD 16-MAY-2002.

XX PF-NOV-2001; 2001WO-EP012933.
 XX 08-NOV-2000; 2000EP-00124418.
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 PA XX Egner R, Winkler D, Roenspeck W, Kunze R;
 PI XX DR WPI; 2002-557447/59.
 PT New immunoglobulin-binding peptides, useful for removing autoantibodies from serum, e.g. for treating rheumatism, also related solid phases.
 PT XX Claim 3; Page 40; 54pp; German.
 PS XX The present invention relates to immunoglobulin binding peptides. These can be used to remove autoantibodies from solutions, particularly autoantibodies associated with autoimmune diseases such as rheumatism, multiple sclerosis and myasthenia gravis, from body fluids. The present sequence is a peptide of the invention.

SQ Sequence 13 AA;
 XX Query Match 41.7%; Score 30; DB 3; Length 13;
 CC Best Local Similarity 41.7%; Pred. No. 3.1e+02;
 CC Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 CC XX Qy 1 CASELGKSTNTF 12
 CC Db 2 CASSIGTNEQF 13
 XX RESULT 9
 ID AAB75626 standard; peptide; 10 AA.
 XX AC AAB75626;
 XX DT 10-APR-2001 (first entry)
 DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.
 XX KW Human; cancer associated antigen precursor; cancer associated antigen;
 KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
 KW vaccine; cancer.
 XX OS Homo sapiens.
 XX PN WO200100874-A2.
 XX PD 04-JAN-2001.
 XX PF 23-JUN-2000; 2000WO-US013207.
 XX PR 30-JUN-1999;
 XX PA (LUDWIG) LUDWIG INST CANCER RES.
 XX PI Sahin U, Tureci O, Pfreundschuh M;
 XX DR WPI; 2001-112465/12.
 XX PT Diagnosing a disorder characterized by expression of a human cancer associated antigen precursor, comprises detecting interaction of an agent with a nucleic acid molecule encoding the antigen precursor.
 XX PS Example 10; Page 62; 126PP; English.
 XX CC The present invention describes a method for diagnosing a disorder characterised by expression of a human cancer associated antigen (CAA) precursor (I) coded by a NA Group 1 nucleic acid molecule (NI) comprising CC contacting the biological sample with an agent (A) that specifically CC binds to N1, (I) or its fragment, complexed with an human leucocyte CC antigen (HLA) molecule and determining the interaction between the agent CC and N1 or (I). (I) has cytostatic activity and can be used in gene CC therapy and vaccine production. The method can be used for treating a CC subject with a condition characterised by expression of (I) in cells of a CC subject. AAB75607 and AAB75608 represent proteins from human cancer CC associated antigen precursors, and AAB75609 to AAB75602 represent HLA CC class I binding motifs in human cancer associated antigen precursors CC given in the exemplification of the present invention
 XX SQ Sequence 10 AA;
 XX Query Match 40.3%; Score 29; DB 4; Length 10;
 CC Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

XX The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains. Compositions which contain autoantigenic peptides binding specifically to XX

XX DR WPI; 1999-571717/4B.
 XX New peptides which selectively home to organs or tissues, used for, e.g., identifying target ligands and for therapy of pathological conditions.
 XX Example 6; Page 144; 193pp; English.

CC The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAY49066 represent sequences which are used in the exemplification of the present invention. (updated on 20-MAR-2003 to correct PR field.)

XX SQ Sequence 9 AA;

Query Match 7 KSTNTFC 13 Score 28; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
 AAB10896 standard; protein; 9 AA.
 AC AAB10896;
 XX DT 26-JAN-2001 (first entry)
 DE Human 9D7 protein immunogenic fragment SEQ ID NO: 55.
 XX Tumor-associated antigen; 9D7; human; cytostatic; immunogenic; immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney; lung; colon; breast; carcinoma; Hodgkin's lymphoma.
 OS Homo sapiens.
 PN DE190950-A1.
 XX PD 07-SEP-2000.
 PF 04-MAR-1999; 99DE-01009503.
 PR 04-MAR-1999; 99DB-01009503.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PI Klade C, Adolf G, Sommergruber W, Heider K;
 DR WPI; 2000-588357/56.
 PT New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer and for producing diagnostic or therapeutic antibodies.

XX Claim 6; Page 45; 50pp; German.

PS This invention describes a novel tumor-associated antigen, designated 9D7 which has cytostatic activity. The invention also describes a method for isolating (a) a polypeptide (I) that includes (S1) as part of its sequence; (b) an immunogenic protein fragment or Peptide (II) derived from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7, (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a protein (IV) with the immunogenic properties of 9D7 or its fragments; (e) a recombinant DNA (VIIIA) that includes (III); and (f) antibodies (Ab) directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use in in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7 can be used similarly and cells that express 9D7 are useful in cellular anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for imaging, diagnosing and monitoring cancers, also, when conjugated to cytotoxins or radiomimic, as therapeutic agents. Peptides derived from 9D7 may also be used diagnostically to test for an immune response. 9D7-associated cancers are particularly kidney, lung, colon and breast carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic fragments of the human tumor-associated antigen 9D7 which is described in the method of the invention

XX Sequence 9 AA;

Query Match 1 CASBLGK 7 Score 28; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CASBLGK 7
 ID AAE26783 standard; peptide; 9 AA.
 AC AAE26783;
 XX DT 13-DEC-2002 (first entry)
 DE Fibrin binding peptide #36.
 XX KW Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis; myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic; anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder; inflammatory disorder; angiogenesis; stroke; cerebroprotective.
 XX Unidentified.
 OS XX
 PN WO200255544-A2.
 XX PD 18-JUL-2002.
 PF 21-DEC-2001; 2001WO-US049534.
 XX PR 23-DEC-2000; 2000US-00747403.
 PA (DYAX-) DYAX CORP.
 PI Wescott CR, Beltz JP, Sato AK;
 XX DR WPI; 2002-666875/71.
 XX PT Novel synthetic fibrin-binding moiety, useful for detecting, imaging, or localizing fibrin-containing clots by magnetic resonance imaging, PT radioimaging and for treating diseases involving thrombus formation e.g. stroke.
 XX PS Claim 4; Page 55; 89pp; English.

CC The invention relates to a synthetic fibrin binding group having affinity for fibrin. The invention is useful for detecting fibrin in a mammalian subject which involves (a) detectably labelling the binding group; (b) administering to the subject the labelled polypeptide, and (c) detecting the labelled polypeptide in the subject. The invention is useful for treating a disease involving thrombus formation e.g. deep-vein thrombosis, pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial infarct, reperfusion ischaemia or stroke. The binding moieties are useful for detection, imaging and localisation of fibrin-containing clots by magnetic resonance imaging, radioimaging and other imaging methods and are also useful in the diagnosis and treatment of coronary conditions where fibrin plays a role. The fibrin binding moieties are useful for

detecting and diagnosing numerous pathophysiologies in which fibrin plays a role e.g. peritoneal adhesions which often occur after surgery or inflammatory and neoplastic processes and are comprised of a fibrin network; fibroblasts, macrophages and new blood vessels; rheumatoid arthritis, lupus or septic arthritis which often have bits of fibrin containing tissues called rice bodies in the synovial fluid of their joints; thrombocytopenic purpura, a type of anaemia in which deposits in arterioles causes turbulent blood flow resulting in stress and destruction of red blood cells. The fibrin specific agents can also be used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain or other organs, as well as the detection of tumours, diabetic retinopathy, early or high-risk atherosclerosis and other autoimmune and inflammatory disorders. Fibrin specific agents also could provide both direct or surrogate markers of disease models in which hypoxia and angiogenesis are expected to play a role. The invention is also useful for screening molecular libraries. The present sequence is a fibrin binding peptide

Sequence 9 AA;

Query Match 38.9%; Score 28; DB 5; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 DB 2 GOESRTFC 9

RESULT 15
 AAB10895 standard; protein; 10 AA.
 ID AAB10895;
 XX AC AAB10895;
 XX DT 26-JAN-2001 (first entry)

XX Human 9D7 protein immunogenic fragment SEQ ID NO: 54.
 DE Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
 KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
 KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.
 XX Homo sapiens.
 OS DE19909503-A1.
 PN XX DR 2000-588357/56.
 PD XX 07-SEP-2000.
 XX PF 04-MAR-1999; 99DE-01009503.
 PR XX 04-MAR-1999; 99DE-01009503.
 XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX PI Klaude C, Adolf G, Sommergruber W, Heider K;
 XX DR
 XX PS Page 45; Sopp; German.

CC This invention describes a novel tumor-associated antigen, designated 9D7 which has cytostatic activity. The invention also describes a method for isolating (a) a polypeptide (I) that includes (S1) as part of its sequence, (b) an immunogenic protein fragment or Peptide (II) derived from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7, (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a protein (IV) with the immunogenic properties of 9D7 or its fragments; (e) a recombinant DNA (IIIa) that includes (III); and (f) antibodies (Ab) directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

peptides, are used to induce a humoral and/or cellular response for use in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7 can be used similarly and cells that express 9D7 are useful in cellular imaging, diagnostics and monitoring cancers, also, when conjugated to cytotoxins or radiionuclides, as therapeutic agents. Peptides derived from 9D7 may also be used diagnostically to test for an immune response. 9D7-associated cancers are particularly kidney, lung, colon and breast carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic fragments of the human tumor-associated antigen 9D7 which is described in the method of the invention

Sequence 10 AA;

Query Match 38.9%; Score 28; DB 3; Length 10;
 Best Local Similarity 71.4%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX SQ Sequence 10 AA;
 QY 1 CASELGK 7
 Db 4 CGRLGK 10

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw mode.

Run on: September 5, 2004, 10:32:02 ; Search time 67 Seconds
 (without alignments)
 61.132 Million cell updates/sec

Title: US-09-761-636A-5
 Perfect score: 72
 Sequence: 1 CASBLGKSTNTFC 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 191768

Minimum DB seq length: 0
 Maximum DB seq length: 13

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgns_6_ptodata/2/pubpa/US07_PUBCOMB.pep:
 2: /cgns_6_ptodata/2/pubpa/BCT_NEW_PUB.pep:
 3: /cgns_6_ptodata/2/pubpa/US06_NEW_PUB.pep:
 4: /cgns_6_ptodata/2/pubpa/US05_PUBCOMB.pep:
 5: /cgns_6_ptodata/2/pubpa/US07_PUBCOMB.pep:
 6: /cgns_6_ptodata/2/pubpa/BCTUS_PUBCOMB.pep:
 7: /cgns_6_ptodata/2/pubpa/US08_NEW_PUB.pep:
 8: /cgns_6_ptodata/2/pubpa/US08_PUBCOMB.pep:
 9: /cgns_6_ptodata/2/pubpa/US09_PUBCOMB.pep:
 10: /cgns_6_ptodata/2/pubpa/US09_PUBCOMB.pep:
 11: /cgns_6_ptodata/2/pubpa/US09_PUBCOMB.pep:
 12: /cgns_6_ptodata/2/pubpa/US09_NEW_PUB.pep:
 13: /cgns_6_ptodata/2/pubpa/US10A_PUBCOMB.pep:
 14: /cgns_6_ptodata/2/pubpa/US10B_PUBCOMB.pep:
 15: /cgns_6_ptodata/2/pubpa/US10C_PUBCOMB.pep:
 16: /cgns_6_ptodata/2/pubpa/US10_NEW_PUB.pep:
 17: /cgns_6_ptodata/2/pubpa/US60_PUBCOMB.pep:
 18: /cgns_6_ptodata/2/pubpa/US60_PUBCOMB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	9 US-09-761-636A-5	Sequence 5, Appli
2	69	95.8	13	9 US-09-761-636A-15	Sequence 15, Appli
3	65	90.3	13	9 US-09-761-636A-16	Sequence 16, Appli
4	65	90.3	13	9 US-09-761-636A-18	Sequence 18, Appli
5	61	84.7	13	9 US-09-761-636A-17	Sequence 17, Appli
6	32	44.4	13	16 US-10-415-665-14	Sequence 14, Appli
7	30	41.7	10	14 US-10-208-304-14	Sequence 14, Appli
8	29	40.3	13	16 US-10-415-665-15	Sequence 15, Appli
9	28	38.9	9	14 US-10-034-974-55	Sequence 55, Appli
10	28	38.9	13	16 US-10-415-665-8	Sequence 8, Appli
11	28	38.9	13	16 US-10-415-665-11	Sequence 11, Appli
12	27	37.5	10	10 US-09-573-822C-626	Sequence 626, App
13	27	37.5	10	14 US-10-271-343-19	Sequence 19, App
14	27	37.5	12	10 US-09-791-393-262	Sequence 262, App
15	27	37.5	12	10 US-09-791-389-262	Sequence 262, App

ALIGNMENTS

RESULT	1	US-09-761-636A-5	;	Sequence 5, Application US/09761636A
			;	PARENTAL INFORMATION:
			;	APPLICANT: ACHEN, Marc
			;	STACHER, Steven
			;	HUGHES, Richard
			;	CENDON, Angela
			;	TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
			;	CURRENT APPLICATION NUMBER: US/09/761-636A
			;	PRIOR APPLICATION NUMBER: US 60/176,293
			;	PRIOR FILING DATE: 2001-01-18
			;	PRIOR APPLICATION NUMBER: US 60/204,590
			;	NUMBER OF SEQ ID NOS: 34
			;	SOFTWARE: Patentin version 3.0
			;	SEQ ID NO 5
			;	LENGTH: 13
			;	TYPE: PRT
			;	ORGANISM: Homo sapiens
			;	US-09-761-636A-5

Query Match Score 72; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.6e-06;
 Matches 13, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13

RESULT 2
 US-09-761-636A-15
 Sequence 15, Application US/09761636A
 ; Patent No. US2002065218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match 95.8%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.2e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 CASELGKSTNTFC 13

RESULT 3
US-09-761-636A-16
Sequence 16; Application US/09761636A
Patent No. US20020065218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

Query Match 90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00011;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 CASELGKSTNTFC 13

RESULT 4
US-09-761-636A-18
Sequence 18; Application US/09761636A
Patent No. US20020065218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
; Binding Immunoglobulins
; FILE REFERENCE: P68842US0
; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: PCT/EP01/12933
 PRIOR FILING DATE: 2001-11-08
 PRIOR APPLICATION NUMBER: EP0124418.5
 PRIOR FILING DATE: 2000-11-08
 NUMBER OF SEQ ID NOS: 88
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 14
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Description of the artificial sequence:
 OTHER INFORMATION: synthetic peptide having affinity for immunoglobulins
 US-10-415-665-14

Query Match 1 CASELGK 7 Score 44.4%; Pred. No. 80; Length 13;
 Best Local Similarity 85.7%;保守性 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CASELGK 7
 Db 2 CASHLGK 8

RESULT 7
 US-10-208-304-14
 Sequence 14, Application US/10208304
 Publication No. US20030124571A1
 GENERAL INFORMATION:
 APPLICANT: Larisch, Sarit
 TITLE OF INVENTION: NOVEL HUMAN SEPTIN AND USES THEREFOR
 FILE REFERENCE: 11613-42USW1
 CURRENT APPLICATION NUMBER: US/10/208,304
 CURRENT FILING DATE: 2002-07-29
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: US 60/178,866
 PRIOR FILING DATE: 2000-01-29
 PRIOR APPLICATION NUMBER: US 60/258,725
 PRIOR FILING DATE: 2000-12-29
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 14
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Drosophila
 US-10-208-304-14

Query Match 1 CASELGK 7 Score 41.7%; Pred. No. 1.4e+02; Length 10;
 Best Local Similarity 87.5%;保守性 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ASELGKST 9
 Db 2 ASGLGKST 9

RESULT 8
 US-10-415-665-15
 Sequence 15, Application US/10415665
 Publication No. US20040087765A1
 GENERAL INFORMATION:
 APPLICANT: Eigner, Ralf
 APPLICANT: Kunze, Rudolf
 APPLICANT: Winkler, Dirk
 APPLICANT: Roenspeck, Wolfgang
 TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for Binding Immunoglobulins

RESULT 9
 US-10-034-974-55
 Sequence 55, Application US/10034974
 Publication No. US0030143159A1
 GENERAL INFORMATION:
 APPLICANT: DYAX CORP.
 APPLICANT: Belitzer, James P.
 APPLICANT: Wescott, Charles R.
 APPLICANT: SATO, Aaron K.
 TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
 FILE REFERENCE: DX-024.1.PCT; DX-04.1.US
 CURRENT APPLICATION NUMBER: US/10/034,974
 CURRENT FILING DATE: 2001-12-21
 PRIOR APPLICATION NUMBER: US 09/747,403
 PRIOR FILING DATE: 2000-12-23
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 55
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: fibrin binding polypeptides
 US-10-034-974-55

Query Match 1 CASELGIK 7 Score 40.3%; Pred. No. 2.7e+02; Length 13;
 Best Local Similarity 71.4%;保守性 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CASELGIK 7
 Db 2 CATHLGK 8

RESULT 10
 US-10-415-665-8
 Sequence 8, Application US/10415665
 Publication No. US20040087765A1
 GENERAL INFORMATION:
 APPLICANT: Eigner, Ralf
 APPLICANT: Kunze, Rudolf
 APPLICANT: Winkler, Dirk
 APPLICANT: Roenspeck, Wolfgang
 TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for Binding Immunoglobulins

```

; FILE REFERENCE: P68842US0
; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/EP01/12933
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: EP00124418.5
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: synthetic peptide having affinity for
; OTHER INFORMATION: immunoglobulins
; US-10-415-665-8

Query Match 38.9%; Score 28; DB 16; Length 13;
Best Local Similarity 71.4%; Pred. No. 4.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CASELGIK 7
Db 2 CAEHIGK 8

RESULT 13
US-10-271-343-19
; Sequence 19, Application US/10271343
; Publication No. US2003016003A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; TITLE OF INVENTION: ON PHAGE
; FILE REFERENCE: 11659.116US1
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3) ..(3)
; OTHER INFORMATION: Xaa is independently Trp, Leu, Val, or Thr
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5) ..(5)
; OTHER INFORMATION: Xaa is D-pro
US-10-271-343-19

Query Match 37.5%; Score 27; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CASELGIK 9
Db 1 CTXEGKL 9

RESULT 14
US-09-573-822C-626
; Sequence 626, Application US/09573822C
; Publication No. US2003019901A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd

Query Match 37.5%; Score 27; DB 10; Length 10;
Best Local Similarity 40.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SELGIKNTF 12
Db 1 AKLSRTTNSF 10

RESULT 14
US-09-791-393-262
; Sequence 262, Application US/09791393
; Publication No. US2003032200A1
; GENERAL INFORMATION:
;
```

APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
 APPLICANT: Parekh, Rajesh Bhikhu
 APPLICANT: Rohlf, Christian
 TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
 TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
 FILE REFERENCE: 2543-1-001 N1
 CURRENT APPLICATION NUMBER: US/09/791,393
 CURRENT FILING DATE: 2002-01-02
 EARLIER APPLICATION NUMBER: GB 0004412.3
 EARLIER FILING DATE: 2000-02-24
 EARLIER APPLICATION NUMBER: GB 0030050.9
 EARLIER FILING DATE: 2000-12-08
 EARLIER APPLICATION NUMBER: US 60/254,830
 EARLIER FILING DATE: 2000-12-12
 NUMBER OF SEQ ID NOS: 308
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO 262
 LENGTH: 12
 TYPE: PRT
 ORGANISM: homo sapien
 US-09-791-393-262

Query Match 37.5%; Score 27; DB 10; Length 12;
 Best Local Similarity 57.1%; Pred. No. 5.7e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CASELGK 7
 Db 6 CTELGR 12

RESULT 15
 US-09-791-389-262
 Sequence 262, Application US/09/791389
 Publication No. US0030032773A1
 GENERAL INFORMATION:
 APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
 APPLICANT: Parekh, Rajesh Bhikhu
 APPLICANT: Rohlf, Christian
 APPLICANT: Terrett, Jonathan Alexander
 APPLICANT: Tyson, Kerry Louise
 TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
 TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
 FILE REFERENCE: 2543-1-001 N2
 CURRENT APPLICATION NUMBER: US/09/791,389
 CURRENT FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: GB 0004412.3
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: GB 0030050.9
 PRIOR FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: US 60/254,830
 PRIOR FILING DATE: 2000-12-12
 NUMBER OF SEQ ID NOS: 308
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO 262
 LENGTH: 12
 TYPE: PRT
 ORGANISM: homo sapien
 US-09-791-389-262

Query Match 37.5%; Score 27; DB 10; Length 12;
 Best Local Similarity 57.1%; Pred. No. 5.7e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CASELGK 7
 Db 6 CTELGR 12

Page blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:29:31 ; Search time 15 seconds
 (without alignments)
 44,743 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGIKSTNTFC 13

Scoring table: BLOSUM62

Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database :	Issued Patents AA:*
1:	/cgn2_6/prodata/2/iaa/5A_COMB_pep:*
2:	/cgn2_6/prodata/2/iaa/5B_COMB_pep:*
3:	/cgn2_6/prodata/2/iaa/6A_COMB_pep:*
4:	/cgn2_6/prodata/2/iaa/6B_COMB_pep:*
5:	/cgn2_6/prodata/2/iaa/PCTUS_COMB_pep:*
6:	/cgn2_6/prodata/2/iaa/backfile1.backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	28	38.9	9	3	US-09-258-754-63	Sequence 63, Appl
2	28	38.9	9	3	US-09-042-107-63	Sequence 63, Appl
3	28	38.9	9	4	US-09-722-250D-63	Sequence 63, Appl
4	27	37.5	13	1	US-09-732-114A-2	Sequence 2, Appl
5	27	37.5	13	1	US-08-110-114A-2	Sequence 2, Appl
6	26	36.1	9	3	US-08-160-092-70	Sequence 70, Appl
7	26	36.1	13	3	US-09-260-513-70	Sequence 70, Appl
8	26	36.1	13	3	US-09-558-754-219	Sequence 219, Appl
9	26	36.1	13	3	US-09-042-107-219	Sequence 219, Appl
10	26	36.1	13	4	US-09-722-250D-219	Sequence 219, Appl
11	26	36.1	13	4	US-09-128-082B-170	Sequence 170, Appl
12	24.5	34.0	12	4	US-08-182-967-12	Sequence 12, Appl
13	24	33.3	7	2	US-08-645-193B-3	Sequence 3, Appl
14	24	33.3	9	6	5247869-110	Patent No. 5247869
15	24	33.3	11	4	US-08-866-545-24	Sequence 24, Appl
16	24	33.3	11	4	US-09-428-082B-116	Sequence 116, Appl
17	24	33.3	11	4	US-09-627-775-24	Sequence 24, Appl
18	24	33.3	13	3	US-09-558-754-183	Sequence 183, Appl
19	24	33.3	13	3	US-09-042-107-183	Sequence 183, Appl
20	24	33.3	13	4	US-08-182-967-11	Sequence 11, Appl
21	24	33.3	13	4	US-09-722-250D-183	Sequence 183, Appl
22	23.5	32.6	11	1	US-09-732-114A-6	Sequence 6, Appl
23	23.5	32.6	11	1	US-08-110-114A-6	Sequence 6, Appl
24	23	31.9	7	2	US-08-445-193B-7	Sequence 7, Appl
25	23	31.9	7	2	US-08-645-193B-59	Sequence 59, Appl
26	23	31.9	9	3	US-08-660-092-150	Sequence 150, Appl
27	23	31.9	9	3	US-08-660-092-151	Sequence 151, Appl

RESULT 1
 US-09-258-754-63
 ; Sequence 63, Application US/09258754
 ; Patent No. 6174697

; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; RAJOTTE, Daniel
 ; PASQUALINI, Renata
 ; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using Membrane Dipeptidase
 ; FILE REFERENCE: P-LJ 3443
 ; CURRENT APPLICATION NUMBER: US/09/258,754
 ; EARLIER APPLICATION NUMBER: 1999-02-26
 ; EARLIER FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 452
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 63
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; LENGTH: 9
 ; US-09-258-754-63

Query Match 38.9%; Score 28; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 3e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 KSTNTTC 13
 :||| |
 Db 3 RSTNTGC 9

RESULT 2
 US-03-042-107-63
 ; Sequence 63, Application US/09042107
 ; Patent No. 6232881

; GENERAL INFORMATION:
 ; APPLICANT: Pasqualini, Renata
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or Tissues
 ; FILE REFERENCE: P-LJ 92
 ; CURRENT APPLICATION NUMBER: US/09/042,107
 ; NUMBER OF SEQ ID NOS: 436
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 63
 ; LENGTH: 9

TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-042-107-63

Query Match Score 28; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 3e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
 Db 3 RSTNTGC 9

RESULT 3
 US-09-722-250D-63
 Sequence 63, Application US/09722250D
 Patent No. 661051
 GENERAL INFORMATION:
 FILE REFERENCE: P-LJ 4514
 APPLICANT: Pasqualini, Renata
 TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
 CURRENT FILING DATE: 2000-11-22
 PRIOR APPLICATION NUMBER: US/09/722,250D
 PRIOR FILING DATE: 1998-03-13
 NUMBER OF SEQ ID NOS: 437
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 63
 LENGTH: 9

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-722-250D-63

Query Match Score 28; DB 4; Length 9;
 Best Local Similarity 71.4%; Pred. No. 3e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
 Db 3 RSTNTGC 9

RESULT 4
 US-07-732-114A-2
 Sequence 2, Application US/07732114A
 Patent No. 5298396
 GENERAL INFORMATION:
 APPLICANT: KOTZIN, BRIAN L.
 APPLICANT: MARRACK, PHILIPPA
 APPLICANT: KAPPLER, JOHN
 APPLICANT: PALIARD, XAVIER
 APPLICANT: PALIARD, XAVIER
 TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson & Bratschun, L.L.C.
 STREET: 8400 E. Prentice Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6.0 (a) For Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/170 114A
 FILING DATE: 20-DECEMBER-1993
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/732,114
 FILING DATE: 18-JULY-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/488,353
 FILING DATE: 2-MARCH-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07,437,370
 FILING DATE: 15-NOVEMBER-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 850-9900
 TELEFAX: (303) 850-9401
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-07-732-114A-2

Query Match 37.5%; Score 27; DB 1; Length 13;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 4;
 Indels 0; Gaps 0;

Qy 1 CASLIGKSTNT 11
 Db 1 CASSLYGTRNT 11

RESULT 5
 US-08-170-114A-2
 Sequence 2, Application US/08170114A
 Patent No. 5776708
 GENERAL INFORMATION:
 APPLICANT: KOTZIN, BRIAN L.
 APPLICANT: MARRACK, PHILIPPA
 APPLICANT: KAPPLER, JOHN
 APPLICANT: PALIARD, XAVIER
 TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson & Bratschun, L.L.C.
 STREET: 8400 E. Prentice Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6.0 (a) For Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/170 114A
 FILING DATE: 20-DECEMBER-1993
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/488,353
 FILING DATE: 2-MARCH-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07,437,370
 FILING DATE: 15-NOVEMBER-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Julie L. Bernard
 REGISTRATION NUMBER: 36,450
 REFERENCE/DOCKET NUMBER: NJH217.3

RESULT 7
 US-09-160-513-70
 Sequence 70, Application US/09160513
 Patent No. 6110775
 GENERAL INFORMATION:
 APPLICANT: Victoria, Edward J.
 ADDRESS: Marquis, David M.
 APPLICANT: Jones, David S.
 APPLICANT: Yu, Lin
 TITLE OF INVENTION: apl IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 9404-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/160,513
 FILING DATE: 1998-DEC-24
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CATHERINE M. POLITZI
 REGISTRATION NUMBER: 40,130
 REFERENCE/DOCKET NUMBER: 25231-20061.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-160-513-70
 Query Match 36.1%; Score 26; DB 4; Length 9;
 Best Local Similarity 71.4%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CASELGK 7
 Db 1 CAGVIGK 7
 RESULT 8
 US-09-258-754-219
 Sequence 219, Application US/09258754
 Patent No. 6174617
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 ADDRESS: Pasqualini, Renata
 APPLICANT: Rajotte, Daniel
 TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
 MOLECULE TYPE: Peptide
 US-08-660-092-70
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/660,092
 FILING DATE: 06-JUN-1996
 CLASSIFICATION: A15
 ATTORNEY/AGENT INFORMATION:
 NAME: Park, Freddie K.
 REGISTRATION NUMBER: 25231-20061.20
 TELEPHONE: (415) 813-5600
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-660-092-70
 Query Match 36.1%; Score 26; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CASELGK 7
 Db 1 CAGVIGK 7

; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-258-754-219

Query Match 36.1%; Score 26; DB 3; Length 13;
 Best Local Similarity 30.8%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 1 CGSHCGQLCKSLC 13

RESULT 9
 ; Sequence 21.9, Application US/09042107
 ; Patent No. 6232387
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; TITLE OF INVENTION: Pasqualini, Renata
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
 ; Tissues
 ; FILE REFERENCE: P-LJ 2892
 ; CURRENT APPLICATION NUMBER: US/09/042,107
 ; CURRENT FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 436
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2119
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-042-107-219

Query Match 36.1%; Score 26; DB 3; Length 13;
 Best Local Similarity 30.8%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 1 CGSHCGQLCKSLC 13

RESULT 10
 ; Sequence 21.9, Application US/09722250D
 ; Patent No. 6161651
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; TITLE OF INVENTION: Pasqualini, Renata
 ; Tissue
 ; FILE REFERENCE: P-LJ 4514
 ; CURRENT APPLICATION NUMBER: US/09/722,250D
 ; CURRENT FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: US 09/042,107
 ; PRIOR FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 437
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2119
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-722-250D-219

Query Match 36.1%; Score 26; DB 4; Length 13;
 Best Local Similarity 30.8%; Pred. No. 3e+02; Indels 7; Mismatches 2; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 1 CGSHCGQLCKSLC 13

RESULT 11
 ; Sequence 170, Application US/09428082B
 ; Patent No. 6660843
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: CHEETHAM, JANET C.
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527
 ; CURRENT APPLICATION NUMBER: US/09/428,082B
 ; CURRENT FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 1133
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 170
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE
 US-09-428-082B-170

Query Match 36.1%; Score 26; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NTFC 13
 Db 8 NTFC 11

RESULT 12
 ; Sequence 12, Application US/08182967
 ; Patent No. 6413316
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Jennie C.C.
 ; APPLICANT: Brostoff, Steven W.
 ; APPLICANT: Carlo, Dennis J.
 ; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/182,967
 ; FILING DATE: 14-JAN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/462,471
 ; FILING DATE: 05-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/813,867
 ; FILING DATE: 14-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/813,867
 ; FILING DATE: 14-DEC-1991

APPLICATION NUMBER: US 07/644,611
 FILING DATE: 22-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/530,229
 FILING DATE: 30-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/382,085
 FILING DATE: 18-JUL-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/382,086
 FILING DATE: 18-JUL-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/326,314
 FILING DATE: 21-MAR-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Kathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-TM 9830
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 STRANGLINEAR
 US-08-182-967-12

Query Match 34.0%; Score 24.5%; DB 4; Length 12;
 Best Local Similarity 63.6%; Pred. No. 5e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 CASELGKSTNT 11
 Db 1 CASSL-NSLNT 10

RESULT 13
 US-08-645-193B-3
 Sequence 3, Application US/08645193B
 Patent No. 5962253
 GENERAL INFORMATION:
 APPLICANT: Kupke, Thomas
 APPLICANT: Gotz, Friedrich
 APPLICANT: Kempfer, Christoph
 APPLICANT: Jung, Gunther
 TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
 TITLE OF INVENTION: Catalyzed by Flavoprotein BpID
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/645,193B
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Edmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0652-1540000
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-645-193B-3

Query Match 33.3%; Score 24; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 STNTFC 13
 Db 1 SENSFc 6

RESULT 14
 5217869-110
 ;Patent No. 5217869
 ;APPLICANT: KAUVAR, LAWRENCE M.
 ;TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
 :REAGENTS
 ;NUMBER OF SEQUENCES: 121
 ;CURRENT APPLICATION DATA:
 ;APPLICATION NUMBER: US/07/255,906
 ;FILING DATE: 11-OCT-1988
 ;SEQ ID NO:110:
 ;LENGTH: 9
 5217869-110

Query Match 33.3%; Score 24; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GKSTNTF 12
 Db 1 GKGSNN 7

RESULT 15
 US-08-866-545-24
 Sequence 24, Application US/08866545
 Patent No. 6265535
 GENERAL INFORMATION:
 APPLICANT: Greene, Mark I.
 APPLICANT: Murali, Ramachandran
 APPLICANT: Takasaki, Wataru
 TITLE OF INVENTION: PEPTIDES AND PEPTIDE ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/866,545
 FILING DATE: 30-MAY-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER:
 FILING DATE:

i ATTORNEY/AGENT INFORMATION:
i NAME: Coruzzi, Laura A
i REGISTRATION NUMBER: 30,742
i REFERENCE/DOCKET NUMBER: 009113-0004-999
i TELECOMMUNICATION INFORMATION:
i TELEPHONE: 650-493-4935
i TELEFAX: 650-493-5556
i TELEX: 66141 PENNIE
i INFORMATION FOR SEQ ID NO: 24;
i SEQUENCE CHARACTERISTICS:
i LENGTH: 11 amino acids
i TYPE: amino acid
i STRANDEDNESS: single
i TOPOLOGY: linear
; MOLECULE TYPE: NO. 6265535E
US-08-866-545-24

Query Match 33.3%; Score 24; DB 3; Length 11;
Best Local Similarity 5.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;

Qy 1 CASPLGK 7
| |||:
Db 2 CRKELGQ 8

Search completed: September 5, 2004, 10:32:42
Job time : 16 secs

GenCore version 5.1.6
 Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:36:12 ; Search time 22 Seconds
 (without alignments)
 34.979 Million cell updates/sec

Title: US-09-761-636A-6
 Perfect score: 46

Sequence: 1 CNBESLIC B

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0
 Maximum DB seq length: 8

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR 78-*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	37.0	6	S29637	jacalin beta-II ch
2	17	37.0	6	I37263	y protein - human (fragment)
3	15	32.6	6	JU0355	C;Species: Homo sapiens (man)
4	15	32.6	7	B39040	C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
5	15	32.6	8	S59622	A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna
6	15	32.6	8	S19288	A;Reference number: PMID:33010631; MUID:93152661; PMID:8427879
7	15	32.6	8	S67165	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
8	14	30.4	6	B31263	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
9	14	30.4	6	S29881	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
10	14	30.4	7	XEYGD	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
11	14	30.4	7	B47594	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
12	13	28.3	5	A3214	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
13	13	28.3	8	A37521	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
14	12	26.1	6	H48394	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
15	12	26.1	7	C34818	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
16	12	26.1	7	A12016	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
17	12	26.1	8	PC1002	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
18	11	23.9	4	A4190	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
19	11	23.9	5	A26330	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
20	11	23.9	5	B22565	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
21	11	23.9	5	A4492	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
22	11	23.9	6	A31263	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
23	11	23.9	7	A58512	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
24	11	23.9	7	A4668	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
25	11	23.9	8	C61512	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
26	11	23.9	8	PT0554	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
27	10	21.7	4	S5237	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
28	10	21.7	5	A60803	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992
29	10	21.7	5	PT0610	R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992

5 SLIC 8

30	10	21.7	6	2	\$11556
31	10	21.7	6	2	\$60293
32	10	21.7	7	2	\$71870
33	10	21.7	7	2	\$08606
34	10	21.7	7	2	B33882
35	10	21.7	7	2	PT0529
36	10	21.7	7	2	\$45648
37	10	21.7	7	2	S09066
38	10	21.7	8	2	D81512
39	10	21.7	8	2	157018
40	10	21.7	8	2	A61597
41	10	21.7	8	2	S29772
42	10	21.7	8	2	157532
43	10	21.7	8	2	A25836
44	9	19.6	3	3	A22565
45	9	19.6	4	2	151049

ALIGNMENTS

RESULT 1					
S29637	jacalin beta-II chain - Artocarpus champeden (fragment)				
C;Species: Artocarpus champeden					
C;Date: 19-Mar-1997					
C;Accession: S29637					
R:Ngoet, L.D.; Brillard, M.; Hoebeke, J.					
Biochim. Biophys. Acta 1156, 219-222, 1993					
A;Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD					
A;Reference number: S29635					
A;Accession: S29637					
A;Molecule type: protein					
A;Experimental source: seed					
C;Complex: heterotetramer; lectin; seed; storage protein					
C;Function:					
A;Description: seed storage protein					
C;Keywords: lectin for β -galactosidase; jacalin; seed; storage protein					
RESULT 2					
Query Match	37.0%	Score 17;	DB 2;	Length 6;	
Best Local Similarity	75.0%	Pred. No. 2.8e+05;			
Matches 3;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	2 NEES 5				
	:				
Db	1 NEQS 4				
RESULT 2					
Y Protein - human (fragment)					
C;Species: Homo sapiens (man)					
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999					
C;Accession: I37263					
R:Waehler, G.; Habener, J.F.;Endocrinology 131, 2010-2015, 1992					
A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna					
A;Reference number: PMID:33010631; MUID:93152661; PMID:8427879					
A;Cross-references: EMBL:X68994; NID:g396171; PID:CAA48780-1; PID:g579816					
C;Genetics:					
A;Gene: CREB					
Query Match					
Best Local Similarity	37.0%	Score 17;	DB 2;	Length 6;	
Matches 3;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	

		RESULT 3					
		JU0355 Lipopeptide WS1279 [validated] - Streptomyces willmorei					
C:Species: Streptomyces willmorei		C:Accession: JU0355 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000					
R:Tsuda, Y.; Okada, M.; Shigenatsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.		Chem. Pharm. Bull. 39, 607-611, 1991					
A:Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial origin		A:Reference number: JU0355; MUID:91300586; PMID:2070441					
A:Accession: JU0355 A:Molecule type: protein		A:Residues: 1-6 <TSU>					
A:Note: the structure was confirmed by synthesis		C:Keywords: blocked amino end; lipoprotein					
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental		F:1/Modified site: fatty acylated amino end (Cys) #status experimental					
Query Match Score 15; DB 2; Length 6;		Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;					
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 1 CN 2 Db 1 CN 2					
RESULT 4		B39040 Calsequestrin, fast skeletal muscle - rabbit (fragment)					
C:Species: Oryctolagus cuniculus (domestic rabbit)		C:Accession: B39040 C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997					
R:Cal, S.E.; Jones, L.R.		J. Biol. Chem. 266, 391-398, 1991					
A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein kinase II		A:Reference number: A39040; MUID:91093153; PMID:1985907					
A:Accession: B39040 A:Status: preliminary		A:Molecule type: protein					
A:Residues: 1-7 <CAL>		A:Keywords: phosphoprotein; skeletal muscle					
Query Match Score 15; DB 2; Length 7;		Best Local Similarity 60.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;					
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		Qy 2 NEESL 6 : Db 2 DEEDL 6					
RESULT 5		S59622 metallothionein isoform a, cadmium-binding - Arianta arbustorum (terrestrial snail) (fra					
C:Species: Arianta arbustorum		C:Accession: S59622 C:Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999					
R:Berger, B.; Hunziker, P.E.; Hauer, C.R.; Dallinger, R.		Biochem. J. 311, 951-957, 1995					
A:Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothioneins		A:Reference number: S59621; MUID:96067616; PMID:7487956					
A:Accession: S59622 A:Molecule type: protein		A:Residues: 1-8 <BER>					
C:Superfamily: metallothionein		C:Keywords: chelation; metal binding; metal-thiolate cluster					
Query Match Score 15; DB 2; Length 8;		Qy 3 EESI 7 Db 4 BEDDV 8					
RESULT 6		S19288 acylase - Kluyvera cryocrescens					
C:Species: Kluyvera cryocrescens		C:Accession: S19288 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997					
R:Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.		Biochem. J. 280, 659-662, 1991					
A:Title: Chemical modification of serine at the active site of penicillin acylase from K.		A:Reference number: S19288 A:Accession: S19288					
A:Molecule type: protein		A:Residues: 1-8 <MAR>					
Query Match Score 15; DB 2; Length 8;		Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;					
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 1 CN 2 Db 1 CN 2					
RESULT 7		S69165 S69165 ferredoxin a2 - Japanese radish (fragment)					
C:Species: Kaiware daikon (Japanese radish)		C:Accession: S69165 C:Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998					
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.		Arch. Biochem. Biophys. 316, 797-802, 1995					
A:Title: Four ferredoxins from Japanese radish leaves.		A:Reference number: S69164; MUID:95168867; PMID:7864635					
A:Accession: S69165 A:Molecule type: protein		A:Residues: 1-8 <OBA>					
C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein		C:Accession: 2Fe-2S; electron transfer; iron-sulfur protein					
Query Match Score 15; DB 2; Length 8;		Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;					
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		Qy 3 EESI 7 Db 4 BEDDV 8					
RESULT 8		B31263 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f.					
C:Species: Plasmodium falciparum		C:Accession: B31263 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996					
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.		Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988					
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase		A:Reference number: A94217; MUID:89057886; PMID:2904149					
A:Accession: B31263 A:Status: not compared with conceptual translation		A:Molecule type: DNA					
A:Residues: 1-6 <PT>		C:Keywords: methyltransferase; NADP; oxidoreductase					
Query Match Score 14; DB 2; Length 6;		Query Match 30.4%; Score 14; DB 2; Length 6;					

Best Local Similarity 60.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1;

Qy 2 NEESL 6 C;Species: Canis lupus familiaris (dog)
Db 2 NWESTI 6 C;Accession: S29881
R;Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Brisbin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A;Title: Structure of three ion-transport adenosine triphosphatases around
A;Reference number: S29881; MUID:85131201; PMID:3156136
A;Accession: S29881
A;Molecule type: protein
A;Residues: 1-6 <WAL>
C;Keywords: ATP; hydrolase; ion transport; phosphoprotein;
F;Active site: Asp (aspartate/phosphate intermediate) #status predicted

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEES 5 C;Accession: A01341
Db 2 CSDKT 6 R;Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A;Reference number: A01341
A;Accession: A01341
A;Molecule type: protein
A;Residues: 1-7 <AVI>
C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, may inactivate the enzyme by binding to its prosthetic copper group.
C;Superfamily: Galactose oxidase inhibitor
C;Keywords: copper

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NEES 5 C;Accession: B47594
Db 4 NTES 7 R;Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.
J. Bacteriol. 175, 4095-4103, 1993
A;Title: Gene structure and expression of the Corynebacterium flavum N13 ask-and operon.
A;Reference number: A47594; MUID:33308089; PMID:8100567
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA

A;Residues: 1-8 <FOU>
C;Keywords: phosphotransferase

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 BESLI 7 C;Accession: A32014
Db 2 BEAVL 6 R;Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A;Title: Identification and characterization of the products from the traJ and traY gene
A;Reference number: A32014; MUID:88227859; PMID:2836369

Query Match 28.3%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NEE 4 C;Accession: A12014
Db 2 NDE 4 R;phycoerythrin gamma-E chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1993
C;Accession: A37521; J22565
P;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:386644
A;Accession: A37521
A;Molecule type: Protein
A;Residues: 1-8 <KLO>

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SLIC 8 C;Accession: H48394
Db 4 ALAC 7 R;primigenius taurinus (cattle)
C;Species: Bos primigenius taurinus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
R;Matther, T.H.; Banghart, J.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470

RESULT 9

S29881

RESULT 12

A32014

RESULT 13

A37521

RESULT 14

H48394

A; Accession: H48394
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-6 <MAT>
A; Experimental source: milk
A; Note: sequence extracted from NCBI backbone (NCBIP:131518)
C; Keywords: glycoprotein

Query Match 26.1%; Score 12; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 ESLIC B
 | |
 DB 2 EULGC 6

RESULT 15

B34818
Vicilin 57K chain - pigeon pea (fragment)
C; Species: Cajanus cajan (pigeon pea)
C; Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C; Accession: B34818
R.Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A; Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A; Reference number: A34818; MUID:90165956; PMID:2300256
A; Accession: B34818
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-7 <MAW>

Query Match 26.1%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CNE 3
 | |
 DB 3 CME 5

Search completed: September 5, 2004, 10:40:20
Job time : 23 secs

Scoring table:	BLOSUM62					
Gapopen:	10.0 , Gapext:					
Searched:	141681 seqs, 52070155 residues					
Total number of hits satisfying chosen parameters:	158					
Minimum DB seq length:	0					
Maximum DB seq length:	8					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing First 45 summaries					
Database :	SwissProt_42:*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	14	30.4	7	1	IGAO_DACDE	P06294 dactylium d
2	13	28.3	5	1	TRM3_ECOLI	P13973 escherichia
3	13	28.3	8	1	PLP_BRANA	P81707 brassica na
4	12	26.1	7	1	UP03_MOUSE	P38641 mus musculus
5	12	26.1	8	1	UPA1_HUMAN	P30087 homo sapien
6	11	23.9	7	1	BRHP_CONTIN	P58803 conus imper
7	11	23.9	8	1	FARI_ASCFSU	P31889 ascaris suu
8	11	23.9	8	1	CAD1_ENTFA	P13268 enterococcus
9	10	21.7	8	1	ACT_CARMA	P80709 carcinus ma
10	9	19.6	6	1	TMOF_SARBU	P41495 sarcophaga
11	9	19.6	8	1	COW2_CONPU	P58785 conus purpu
12	9	19.6	8	1	GLDR_HUMAN	P02729 homo sapien
13	8	17.4	6	1	ACPH_RABIT	P25154 oryctolagus
14	8	17.4	6	1	ASP2_LACSN	P82655 lactobacillus
15	8	17.4	7	1	CCP1_ENTFA	P20104 enterococcus
16	8	17.4	7	1	FARI_PROCL	P38499 procamburus
17	8	17.4	7	1	GFRP_MOUSE	P99025 mus musculus
18	8	17.4	7	1	WWA1_ACHFEU	P35919 achatina fu
19	8	17.4	7	1	WWA3_ACHFEU	P35921 achatina fu
20	8	17.4	8	1	FAR4_HONAM	P41487 homarus ame
21	8	17.4	8	1	FAR8_CALVO	P41863 calliphora
22	7	15.2	7	1	FAR2_ASCFSU	P31890 ascaris suu
23	7	15.2	7	1	UH11_RAT	P56576 rattus norvegicus
24	7	15.2	8	1	CLP_THICLU	P80488 thiobacillus
25	7	15.2	8	1	CPD1_ENTFA	P13269 enterococcus
26	7	15.2	8	1	PPK3_PSEAM	P82618 periplaneta
27	7	15.2	8	1	UR09_RAT	P56575 rattus norvegicus
28	7	15.2	8	1	WPL_FERAT	P83195 perkinsus a
29	6	13.0	4	1	EOST_HUMAN	P02731 homo sapien
30	6	13.0	4	1	FURN_ANTEL	P58707 anthropoidea
31	6	13.0	5	1	TPIS_CANFA	P54714 canis familiaris
32	6	13.0	5	1	UXA4_CHLIFRA	P38005 chlamydiae
33	6	13.0	6	1	FARP_MONEX	P41966 moniezia ex

ALIGNMENTS						
RESULT 1						
IGAO_DACDE	ID	IGAO_DACDE	STANDARD;	PRT;	7 AA.	
AC	AC	P06254;	DT 01-JAN-1988 (Rel. 06, Created)	RT 01-JAN-1988 (Rel. 06, Last sequence update)	DB Galactose oxidase inhibitor.	
OS Dactylium dendroides (Cladobotryum dendroides)	OS	OC Eukaryota; Fungi; Ascomycota; Pezizomycetes; Sordariomycetes; Hypocreomycetidae; Ascomycetae; Hypocreaceae; Hypomyces.	OX NCBI_TaxID=5132;	OX [1] RN [1]	RP SEQUENCE.	
RESULT 2						
RA Avigad G.; Markus Z.;	RA	"Identification of a peptide inhibitor of galactose oxidase from Dactylium dendroides.";	RT Ped. Proc. 31:447-447(1972).	RT	CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the galactose oxidase apoenzyme. It may inactivate the enzyme by binding to its prosthetic copper group.	
DR PIR: A01341; XYDGD,	DR	KW Copper; Metalloenzyme inhibitor.	DR KW SEQUENCE 7 AA; 706 MW; 75B01A456D87DB0 CRC64;	DR	CC Query Match Similarity 30.4%; Score 14; DB 1; Length 7; Best Local Similarity 75.0%; Pred. No. 1.4e+15; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
CC Qy 2 NEES 5	Qy	Db 4 NTES 7	Db	CC Qy DR Sequence FROM N.A. ID TRM3_ECOLI STANDARD; PRT; 5 AA.	CC AC P13973; DT 01-JAN-1990 (Rel. 13, Created)	CC AC P13973; DT 01-JAN-1990 (Rel. 13, Last sequence update)
CC RN [1] —	CC RN [1] —	CC RN [1] —	CC RN [1] —	CC RN [1] —	CC RN [1] —	CC RN [1] —
RESULT 3						
ECOLI	ID	TRM3_ECOLI	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN TRAM	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 4						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 5						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 6						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 7						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 8						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 9						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 10						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 11						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 12						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 13						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 14						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 15						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 16						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 17						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 18						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 19						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 20						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 21						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 22						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;	5 AA.	
AC	AC	P13973;	DT 01-JAN-1990 (Rel. 13, Created)	DT 01-JAN-1990 (Rel. 13, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
GN	GN	DE TRAM protein (Fragment).	OS Escherichia coli.	OS Plasmid IncFII R100.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
OG	OG	OG	OG	OG	OG	
RESULT 23						
ENTEROCOCCUS	ID	ENTEROCOCCUS	STANDARD;	PRT;</		

PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the traw family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; M20941; ; NOT_ANNOTATED_CDS.

DR PIR; A32014; A32014.

KW Conjugation; Plasmid; DNA-binding.

FT NON_TER 1 1

SEQUENCE 5 AA; 634 MW; 6B1BAA443500000 CRC64;

Query Match Score 13; DB 1; Length 5;

Best Local Similarity 28.3%; Pred. No. 1.e+05;

Matches 2; Conservative 1; N mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4

DB 2 NDE 4

DNB 2 NDI 4

DNB 2 NFE 4

DNB 2 NHE 4

DNB 2 NLE 4

DNB 2 NRE 4

DNB 2 NSE 4

DNB 2 NTE 4

DNB 2 NVE 4

DNB 2 NWE 4

DNB 2 NZE 4

RN [1]

RP SEQUENCE.

RC STRAIN=CV: TOPAZ; TISSUE=Tapetum;

RX MEDLINE=9309136; PubMed=10120651;

RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,

RA Murphy D.J.;

RT "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of *Brassica napus*.";

PLANTA 208:588-598(1999).

RL FUNCTION: May play a structural role in the elaioplast, a tapetum-

CC specific plastidial lipid organelle.

CC -!- TISSUE SPECIFICITY: Tapetum of anthers.

CC NON_TER 8 8

SEQUENCE 8 AA; 989 MW; 9D7B1AA4522CA042 CRC64;

Query Match Score 13; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.e+05;

Matches 2; Conservative 1; N mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4

DB 2 NDE 4

DNB 2 NDI 4

DNB 2 NFE 4

DNB 2 NHE 4

DNB 2 NLE 4

DNB 2 NRE 4

DNB 2 NSE 4

DNB 2 NTE 4

DNB 2 NVE 4

DNB 2 NWE 4

DNB 2 NZE 4

RN [1]

RP SEQUENCE.

RC STRAIN=CV: TOPAZ; TISSUE=Tapetum;

RX MEDLINE=9309136; PubMed=10120651;

RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,

RA Murphy D.J.;

RT "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of *Brassica napus*.";

PLANTA 208:588-598(1999).

RL FUNCTION: May play a structural role in the elaioplast, a tapetum-

CC specific plastidial lipid organelle.

CC -!- TISSUE SPECIFICITY: Tapetum of anthers.

CC NON_TER 8 8

SEQUENCE 8 AA; 944 MW; C01772C455BB06DA_CRC64;

Query Match Score 13; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.e+05;

Matches 2; Conservative 1; N mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4

DB 2 NDE 4

DNB 2 NDI 4

DNB 2 NFE 4

DNB 2 NHE 4

DNB 2 NLE 4

DNB 2 NRE 4

DNB 2 NSE 4

DNB 2 NTE 4

DNB 2 NVE 4

DNB 2 NWE 4

DNB 2 NZE 4

RN [1]

RP SEQUENCE.

RC STRAIN=CV: TOPAZ; TISSUE=Tapetum;

RX MEDLINE=9309136; PubMed=10120651;

RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,

RA Murphy D.J.;

RT "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of *Brassica napus*.";

PLANTA 208:588-598(1999).

RL FUNCTION: May play a structural role in the elaioplast, a tapetum-

CC specific plastidial lipid organelle.

CC -!- TISSUE SPECIFICITY: Tapetum of anthers.

CC NON_TER 8 8

SEQUENCE 8 AA; 944 MW; C01772C455BB06DA_CRC64;

Query Match Score 13; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.e+05;

Matches 2; Conservative 1; N mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4

DB 2 NDE 4

DNB 2 NDI 4

DNB 2 NFE 4

DNB 2 NHE 4

DNB 2 NLE 4

DNB 2 NRE 4

DNB 2 NSE 4

DNB 2 NTE 4

DNB 2 NVE 4

DNB 2 NWE 4

DNB 2 NZE 4

DNB 2 NZE 4

DNB 2 NZE 4

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.

[1] RN NCBI_TaxID=35631;

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=V; venom;

RX MEDLINE=97184108; PubMed=9030520;

RA Craig A.G.; Jimenez E.C.; Dykert J.J.; Nielsen D.B.; Guiyas J.,
 Abogadie F.C.; Porter J.; Rivier J.E.; Cruz L.J.; Olivera B.M.,
 McIntosh J.M.; RT "A novel post-translational modification involving bromination of
 trypophan. Identification of the residue, L-6-bromotryptophan, in
 peptides from Conus imperialis and Conus radiatus venom.";

RL J. Biol. Chem. 272:4689-4698 (1997).
 CC -!- FUNCTION: Does not elicit gross behavioral symptoms when injected
 centrally or peripherally in mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- MASS SPECTROMETRY: MN=853.19; METHOD=LSIMS.

DR PIR512; A5512.

KW Bromination; Amidation; Pyrrolidone carboxylic acid.

FT DISULFID 2 7 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 1 1 BROMINATION.

FT MOD RES 6 6 AMIDATION.

SQ SEQUENCE 7 AA; 795 MW; 6E37DC6D87EA6B0 CRC64;

Query Match 1 CNE 3 Score 11; DB 1; Length 7;

Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2 CGQ 4

Query Match 7 AA; 953 MW; 69340055CB144350 CRC64;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 7 AA; 953 MW; 69340055CB144350 CRC64;

Query Match 2 NE 3 Score 11; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 2 NE 3 Score 10; DB 1; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Db 2 NE 3

Query Match 2 NE 3 Score 10; DB 1; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Db 2 NE 3

RESULT 8
 CAD1_ENTFA STANDARD; PRT; 8 AA.

CAD1_ENTFA ID CAD1_ENTFA STANDARD; PRT; 8 AA.

AC P13285; DT 01-JAN-1990 (Rel. 13, Created)

AC P13285; DT 01-JAN-1990 (Rel. 13, Last sequence update)

AC P13285; DT 01-FEB-1991 (Rel. 17, Last annotation update)

DB Sex pheromone CAD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI_TaxID=1351;

RN [1] _ TaxID=1351;

RP SEQUENCE;

RX MEDLINE=85051889; PubMed=6437872;

RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C., Craig R.A., Clewell D.B., Suzuki A.;

RA "Isolation and structure of the bacterial sex pheromone, CAD1, that induces plasmid transfer in Streptococcus faecalis.";

RL FEBS Lett. 178:97-100 (1984).

CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PAB1.

KW Pheromone.

SQ SEQUENCE 8 AA; 819 MW; 047DD732C735BB9C7 CRC64;

Query Match 5 SLI 7 Score 23.9%; Score 11; DB 1; Length 8;

Best Local Similarity 66.4%; Pred. No. 1.4e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 3 SLI 5

RESULT 9
 ACT_CARMA STANDARD; PRT; 8 AA.

ACT_CARMA ID ACT_CARMA STANDARD; PRT; 8 AA.

AC P80799; DT 01-OCT-1996 (Rel. 34, Created)

AC P80799; DT 01-OCT-1996 (Rel. 34, Last sequence update)

AC P80799; DT 15-JUL-1999 (Rel. 38, Last annotation update)

DB Actin (Fragment).

OS Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Bivalvia; Decapoda; Pleocyemata; Brachyura;

OC Subbrachyura; Portunoidea; Portunidae; Carcinus;

NCBI_TaxID=6759;

RN [1] _ TaxID=6759;

RP SEQUENCE;

RA Lachaise F., Somme G., Carpenter G., Granjeon E., Webster S., Baghdassarian D.;

RA "A transaldolase. An enzyme implicated in crab steroidogenesis.";

RL Endocrine 5:23-32 (1996).

CC -!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:

CC 6.8. ITS MW IS: 46 kDa.

CC -!- SIMILARITY: Belongs to the actin family.

CC DR InterPro; IPR004000; Actin.

DR InterPro; IPR004000; Actin-like.

DR PROSITE; PS00406; ACTINS_1; PARTIAL.

DR PROSITE; PS00432; ACTINS_2; PARTIAL.

DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.

KW Structural protein.

FT NON_TER 1 1

FT SEQUENCE 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;

Query Match 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Db 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;

Query Match 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

RT unblocking with N-acylaminoacyl-peptide hydrolase.";

RL Anal. Biochem. 199:45-50(1991).

CC -!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal peptide bond of an N-acetylated peptide to generate an N-acetylated amino acid and a peptide with a free N-terminus. It preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.

CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid + peptide.

CC -!- SUBUNIT: Homotetramer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to peptidase family S9C.

MEROPS: S09.004; -

DR PIR: A49792; A49792.

DR PROSITE: PS00708; PRO-ENDOPEP_SER; PARTIAL.

KW Hydrolase; Acetylation.

FT MOD_RES 1 1 ACETYLATION.

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 775 MW; 6732D6C4OB16F000 CRC64;

Query Match Score 8; DB 1; Length 6;

Best Local Similarity 20.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EESLI 7

Db 2 ERQVL 6

RESULT 14

ASP2_LACSN STANDARD PRT; 6 AA.

ID ASP2_LACSN

AC PB2655;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Acid shock protein 2 (Fragment)

OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus

NCBI_TaxID=1625;

RN [1]

RP SEQUENCE.

RC STRAIN=CBL

RX MEDLINE=23322712; PubMed=11429463;

RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;

RT "The acid stress response in Lactobacillus sanfranciscensis CBL.";

RL Microbiology 147:1863-1873 (2001).

CC -!- INDUCTION: Overexpressed in acid environments.

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match Score 8; DB 1; Length 6;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NE 3

Db 5 ND 6

RESULT 15

CCF1_ENTFA STANDARD PRT; 7 AA.

ID CCF1_ENTFA

AC P20104;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DB Sex pheromone ccf10.

OS Enterococcus faecalis (Streptococcaceae; Enterococcus).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

NCBI_TaxID=1351;

[1]

RP SEQUENCE.

RX MEDLINE=89008313; PubMed=3139558;

RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Adsit J.C., Dunn G.M., Suzuki A.;

RT "Structure of CCF10, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline resistance plasmid, pCF10.";

RT J. Biol. Chem. 263:14574-14578(1988).

RL J.-I. FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYIN PLASMID PCF10.

CC DR PIR; A30812; A30812.

KW Pheromone.

SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match Score 8; DB 1; Length 7;

Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SLI 7

Db 3 TIV 5

Search completed: September 5, 2004, 10:38:49

Job time : 16 secs

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:35:32 ; Search time 57 Seconds

(without alignments)

44.283 Million cell updates/sec

Perfect score: 46

Sequence: 1 CNBESLIC 8

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacterioplasm:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	18	39.1	8 10	Q9BF87	dioscorea t	Q9BF87 dioscorea t
2	16	34.8	7 12	Q6713	influenzavirus	Q6713 influenza
3	16	34.8	7 13	Q42564	fugu rubripinnatus	Q42564 fugu rubripinnatus
4	14	30.4	8 4	Q8IV87	homo sapiens	Q8IV87 homo sapiens
5	13	28.3	7 11	Q55184	rattus norvegicus	Q55184 rattus norvegicus
6	13	28.3	8 2	Q32560	escherichia coli	Q32560 escherichia coli
7	12	26.1	8 2	Q2ZEZ9	buchnera apiculata	Q2ZEZ9 buchnera apiculata
8	12	26.1	8 4	Q9BYYS	homo sapiens	Q9BYYS homo sapiens
9	12	26.1	8 4	Q15895	homo sapiens	Q15895 homo sapiens
10	12	26.1	8 4	Q15890	homo sapiens	Q15890 homo sapiens
11	12	26.1	8 6	Q9BF82	arctocephalus	Q9BF82 arctocephalus
12	12	26.1	8 6	Q9BF25	macropus europaeus	Q9BF25 macropus europaeus
13	12	26.1	8 6	Q9BF90	tragelaphus strepsiceros	Q9BF90 tragelaphus strepsiceros
14	12	26.1	8 6	Q9BF81	echinops teucrium	Q9BF81 echinops teucrium
15	12	26.1	8 6	Q9BF93	megaptera novaeangliae	Q9BF93 megaptera novaeangliae
16	12	26.1	8 6	Q9BF81	atelles fasciatus	Q9BF81 atelles fasciatus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	18	39.1	8 10	Q9BF87	dioscorea t	Q9BF87 dioscorea t
2	16	34.8	7 12	Q6713	influenzavirus	Q6713 influenza
3	16	34.8	7 13	Q42564	fugu rubripinnatus	Q42564 fugu rubripinnatus
4	14	30.4	8 4	Q8IV87	homo sapiens	Q8IV87 homo sapiens
5	13	28.3	7 11	Q55184	rattus norvegicus	Q55184 rattus norvegicus
6	13	28.3	8 2	Q32560	escherichia coli	Q32560 escherichia coli
7	12	26.1	8 2	Q2ZEZ9	buchnera apiculata	Q2ZEZ9 buchnera apiculata
8	12	26.1	8 4	Q9BYYS	homo sapiens	Q9BYYS homo sapiens
9	12	26.1	8 4	Q15895	homo sapiens	Q15895 homo sapiens
10	12	26.1	8 4	Q15890	homo sapiens	Q15890 homo sapiens
11	12	26.1	8 6	Q9BF82	arctocephalus	Q9BF82 arctocephalus
12	12	26.1	8 6	Q9BF25	macropus europaeus	Q9BF25 macropus europaeus
13	12	26.1	8 6	Q9BF90	tragelaphus strepsiceros	Q9BF90 tragelaphus strepsiceros
14	12	26.1	8 6	Q9BF81	echinops teucrium	Q9BF81 echinops teucrium
15	12	26.1	8 6	Q9BF93	megaptera novaeangliae	Q9BF93 megaptera novaeangliae
16	12	26.1	8 6	Q9BF81	atelles fasciatus	Q9BF81 atelles fasciatus

RESULT 1

Q9SAY7

ID Q9SAY7

PRELIMINARY;

PRT;

8 AA.

SEQUENCE FROM N.A.

RC STRAIN=DPL7-1;

RX MEDLINE=20279211; PubMed=10821191;

RA Teruchi R., Kahl G.;

RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking

regions of Pal and Pgi genes from Yams (Dioscorea).";

RL Mol. Gen. Genet. 263:554-560(2000).

DR GO:0016855; Fisomerase activity: IEA.

DR GO:00016716; BAA2235.1; -.

DR GO:00016855; Fisomerase activity: IEA.

RN [1] TaxID=64475;

RN SEQUENCE FROM N.A.

RC STRAIN=DPL7-1;

RX MEDLINE=20279211; PubMed=10821191;

RA Teruchi R., Kahl G.;

RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking

regions of Pal and Pgi genes from Yams (Dioscorea).";

RL Mol. Gen. Genet. 263:554-560(2000).

Query Match 39.1%; Score 18; DB 10; Length 8;

Best Local Similarity 75.0%; Pred. No. 1e+06;

Mismatches 1; Conservative 1; Matches 3; Gaps 0;

Indels 0; Del 0; Insert 0;

SLIC 5;

TLIC 8;

RESULT 2

Q67113

ID Q67113

PRELIMINARY;

PRT;

7 AA.

ALIGNMENTS

Q9BF87

Q9BF89

Q9BF88

Q9BF85

Q9BF95

Q9BF99

Q9BF84

Q9BF89

Q9BF96

Q9BF87

Q9BF89

Q9BF88

Q9BF85

Q9BF92

Q9BF7

Q9BF91

Q9BF84

Q9BF89

Q9BF87

Q9BF89

Q9BF88

Q9BF85

Q9BF95

Q9BF99

Q9BF84

Q9BF89

AC Q67113; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end
 DE (Fragment).
 OS Influenzavirus A.
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OC NCBI_TaxID=197911;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=81001892; PubMed=7407922;
 RX Dhar R., Chanock R.M., Lai C.-J.;
 RA "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
 viral mRNA deduced from cloned complete genomic sequences.";
 RT Cell 21:495-500(1980)
 DR EMBL: M25045; AAA43202; 1; -
 FT NON-TER 1 1
 SQ SEQUENCE 7 AA; 834 MW; 605BB0544EA40030 CRC64;
 Query Match 34.8%; Score 16; DB 12; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e-06;
 Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Qy 1 CMEESLIC 8
 Db 3 CN---IC 6
 RESULT 3
 O02564 PRELIMINARY; PRT; 7 AA.
 ID 042564
 AC 012564;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN SCN8A.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoleosteoi;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 NCBI_TaxID=31033;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Maisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U07673; AA080916; -.
 DR GO:GO:0005216; F:ion channel activity; IBA.
 KW Ionic channel.
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
 Query Match 34.8%; Score 16; DB 13; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1e-06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 LIC 8
 Db 3 LVC 5
 RESULT 4
 Q8IVV7 PRELIMINARY; PRT; 8 AA.
 ID Q8IVV7
 AC Q8IVV7;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit
 DE 2-like (Aminotransferase 2), variant 1) (Fragment).
 GN SPTLC2L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith M.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL05020; CAD54807.1; -.
 DR GO:GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON-TER 1 1
 SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEBO42 CRC64;
 Query Match 30.4%; Score 14; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 LIC 8
 Db 1 VIC 3
 RESULT 5
 O05184 PRELIMINARY; PRT; 7 AA.
 ID 005184
 AC 055184;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DR 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Orphan receptor TR4-NS (Fragment).
 RA TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Rodentia; Sciurognathi; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96198747; PubMed=8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RA "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain";
 RT Endocrinology 137:1562-1571(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96239786; PubMed=8661150;
 RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
 RT "New variants of the human and rat nuclear hormone receptor, TR4:
 expression and chromosomal localization of the human gene.";
 RL Genomics 35:361-366(1996).
 DR EMBL; U59454; AAB91433.1; -.
 DR GO:GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON-TER 1 1
 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787BB05350 CRC64;
 Query Match 28.3%; Score 13; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 IC 8
 Db 2 IC 3

RESULT 6
 032560 ID PRELIMINARY; ERT: 8 AA.
 AC 032560;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE "The tdc gene in Escherichia coli W3110 is separated from the rest of the tdc operon by insertion of ISS elements.";
 RN [1] _TaxID=562;
 RA Hesslinger C.; Sawers G.;
 RT "The tdc gene in Escherichia coli W3110 is separated from the rest of the tdc operon by insertion of ISS elements.";
 RL DNA Seq. 9:183-188 (1998).
 DR AJ001620; CA0A0875_1;
 GO; GO:0016301; F:kinase activity; IEA.
 KW Kinase.
 FT NON_TER
 SEQUENCE 8 AA; 1000 MW;
 STRAIN=W3110;
 RX MEDLINE=99449059; PubMed=10520749;
 RA "The tdc gene in Escherichia coli W3110 is separated from the rest of the tdc operon by insertion of ISS elements.";
 RN [1] _TaxID=562;
 RA O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618 (2001).
 DR AY011664; AAG7575_1;
 GO; GO:0005634; C:nucleus; NAS.
 GO; GO:0003677; F:DNA binding; NAS.
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 SQ NON_TER 1
 SEQUENCE 8 AA; 1006 MW;
 DF02C331EEAB572A CRC64;

Query Match 26.1%; Score 13; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IC 8
 Db 5 IC 6

RESULT 7
 Q9ZET9 ID PRELIMINARY; PRT; 8 AA.
 AC Q9ZET9;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
 RN [1] _TaxID=9;
 RA Buchnera aphidicola.
 RA Plasmid pBRC1.
 RA Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 RN SEQUENCE FROM N.A.
 RX MEDLINE=992028304; PubMed=9812361;
 RA Silva P.J.; Van Ham R.C.H.J.; Sabater B.; Latorre A.;
 RT "Structure and evolution of the leucine plasmids carried by the endosymbiont (Buchnera aphidicola) from aphids of the family Aphidiidae.";
 RT FEMS Microbiol. Lett. 168:43-49 (1998).
 RL EMBL; AJ006874; CA07290_1;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:003852; F:2-isopropylmalate synthase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 KW Lyase; Plasmid.
 FT NON_TER 8
 SEQUENCE 8 AA; 917 MW;
 FE205042D6C5B446 CRC64;

Query Match 26.1%; Score 12; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

Qy 2 NEESLI 7
 Db 5 KSLV 8

OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
 OX NCBI_TaxID=9370;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618 (2001).
 DR EMBL: AY011632; AAGG47547.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 978 MW; DF1DD331BEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LIC 8
 Db 2 LYC 4

RESULT 15

Q9BF93 Q9BF93 PRELIMINARY; PRT; 8 AA.
 ID Q9BF93;
 AC Q9BF93;
 DT 01-JUN-2001 (TREMBLref. 17, Created)
 DT 01-JUN-2001 (TREMBLref. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLref. 17, Last annotation update)
 DE CAMP responsive element moderator (Fragment).
 GN CREM.

OS Megaptera novaengliae (Humpback whale).
 OC Balaenopteridae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Megaptera.
 RN NCBI_TaxID=9773;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618 (2001).
 DR EMBL: AY011669; AAGG47580.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LIC 8
 Db 2 LYC 4

Search completed: September 5, 2004, 10:39:53
 Job time : 58 secs

This Page Blank (uspto)

Result No.	Score	Query	Match	Length	DB	ID	Description
1	46	100.0	8	4	AAU04525		Aau0525 VEGF base
2	43	93.5	8	4	AAU04539		Aau0539 VEGF base
3	42	91.3	8	4	AAU04541		Aau0541 VEGF base
4	41	89.1	8	4	AAU04538		Aau0538 VEGF base
5	39	84.8	8	4	AAU04540		Aau0540 VEGF base
6	30	65.2	8	2	AAR24954		Aar24954 Conformat
7	30	65.2	8	3	AAU54526		Aay54526 Human CD4
8	26	56.5	8	2	AAR73351		Aar73351 Human TSH
9	26	56.5	8	2	AAR73350		Aar73350 Human TSH
10	26	56.5	8	3	AAY57040		Aay57040 Feline im
11	26	56.5	8	4	AAU08451		Aau0451 Peptide A
12	25	54.3	8	2	AAR80365		Aar80365 Protein P
13	25	54.3	8	2	AARW49750		Aaw49750 Glutamine
14	25	54.3	8	2	AAY48614		Aay48614 Membrane
15	25	54.3	8	5	ABG35021		Abg35021 Endosatii
16	24	52.2	8	4	AAU08460		Aau0460 Peptide C
17	23	50.0	7	2	AAW25915		Aaw25915 Beta-2-mi
18	23	50.0	8	2	AAR73349		Aar73349 Human TSH
19	23	50.0	8	2	AAR73348		Aar73348 Human TSH
20	23	50.0	8	2	AARW12848		Aarw12848 RGD-bind
21	23	50.0	8	2	AAY48852		Aay48852 Membrane
22	23	50.0	8	2	AAY48662		Aay48662 Membrane
23	23	50.0	8	2	AAY48640		Aay48640 Membrane
24	23	50.0	8	3	AAB06526		Aab06526 Claudin-2
25	23	50.0	8	3	AAB17353		Aab17353 Integrin-

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides), and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangiomata, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 8 AA:

Query Match 100.0%; Score 46; DB 4; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8

Db 1 CNERSLIC 8

PT residues.
XX Example 25; Page 47; 102pp; English.

CC The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VBGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy, hemangiomata, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

SQ Sequence 8 AA:

Query Match 93.5%; Score 43; DB 4; Length 8;
Best Local Similarity 87.5%; Prod. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CNEESLIC 8
Db 1 CNEETLIC 8

RESULT 3

AAU04541

DE VEGF based monocyclic peptide 19.

ID AAU04541 standard; peptide; 8 AA.
XX
AC AAU04539;
XX
DT 26-SEP-2001 (first entry)
DE VEGF based monocyclic peptide 17.
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
OS Synthetic.
PH Location/Qualifiers
FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
XX WO200152875-A1.
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
PA (LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackler S, Cendron A;
DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

PT Location/Qualifiers
FH Key
FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX
PN 26-JUL-2001.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.

PA	(LUDW-) LUDWIG INST CANCER RES.	PN	WO200152875-A1
XX	Achen MG, Hughes RA, Stackler S, Cendron A;	XX	
PI		PD	26-JUL-2001.
XX		XX	18-JAN-2001; 2001WO-US001533.
DR	WPI: 2001-442248/47.	PF	
XX		XX	
PT	Novel monomeric monocyclic peptide, used to interfere with angiogenesis,	PR	18-JAN-2000; 2000US-0176293P.
PT	or lymphangiogenesis, is produced by cyclizing a peptide loop fragment	PR	16-MAY-2000; 2000US-0204590P.
PT	from an exposed loop of a growth factor protein by oxidizing the cysteine	XX	
PT	residues.	PA	(LUDW-) LUDWIG INST CANCER RES.
XX		XX	
PS	Example 25; Page 47; 102pp; English.	PI	Achen MG, Hughes RA, Stackler S, Cendron A;
XX		XX	
CC	The sequence represents a monomeric monocyclic peptide of the invention,	DR	WPI; 2001-442248/47.
CC	whose 3-dimensional structure is modelled on the exposed loop of human	XX	
CC	VEGFD (vascular endothelial growth factor). The invention relates to a	XX	
CC	method of producing a monomeric monocyclic peptide by a measuring beta-	PT	beta carbon separation distances on opposite antiparallel strands of a
CC	peptide loop fragment from an exposed loop of a growth factor protein and	PT	peptide loop fragment from an exposed loop of a growth factor protein by
CC	from an exposed loop of a growth factor protein and	PT	oxidising the peptide by oxidising the cysteine residues.
CC	cyclising the peptide by oxidising the cysteine residues. The monomeric	XX	PT residues.
CC	peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic	PS	Example 25; Page 47; 102pp; English.
CC	peptides) and a cyclic peptide with at least one amino acid deleted prior	XX	
CC	to cyclisation are used to interfere with angiogenesis,	CC	The sequence represents a monomeric monocyclic peptide of the invention,
CC	neovascularisation or lymphangiogenesis in a mammal with a condition	CC	whose 3-dimensional structure is modelled on the exposed loop of human
CC	characterised by angiogenesis, neovascularisation or lymphangiogenesis.	CC	VEGFD (vascular endothelial growth factor). The invention relates to a
CC	The condition is diabetic retinopathy, psoriasis, arthropathy,	CC	method of producing a monomeric monocyclic peptide by a measuring beta-
CC	hemangioma, vascularised malignant or benign tumour, post-recovery	CC	beta carbon separation distances on opposite antiparallel strands of a
CC	cerebrovascular accident, post-angioplasty restenosis, head, heat or cold	CC	peptide loop fragment from an exposed loop of a growth factor protein and
CC	trauma, substance-induced neovascularisation of the liver, excessive	CC	cyclising the peptide by oxidising the cysteine residues. The monomeric
CC	hormone-related angiogenic dysfunction, diabetes induced neovascular	CC	peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC	sequela, hypertension induced neovascular sequelae, or chronic liver	CC	peptides) and a cyclic peptide with at least one amino acid deleted prior
CC	infection. The peptides are also used to modulate vascular permeability	CC	to cyclisation are used to interfere with angiogenesis.
CC	in a mammal (the mammal has a condition characterised by fluid	CC	CC neovascularisation or lymphangiogenesis.
CC	accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,	CC	CC neovascularisation or lymphangiogenesis.
CC	or brain. The peptides are used to image blood vessels and lymphatic	CC	CC whose 3-dimensional structure is modelled on the exposed loop of human
CC	vasculature. The monomeric and bicyclic peptides are used to interfere	CC	VEGFD (vascular endothelial growth factor). The invention relates to a
CC	with at least one biological activity induced by VEGF, VEGF-C or -D and	CC	method of producing a monomeric monocyclic peptide by a measuring beta-
CC	are also used in combination with an anti-inflammatory agent, to treat a	CC	beta carbon separation distances on opposite antiparallel strands of a
CC	chronic inflammation, especially rheumatoid arthritis, psoriasis and	CC	peptide loop fragment from an exposed loop of a growth factor protein and
CC	diabetic retinopathy	CC	cyclising the peptide by oxidising the cysteine residues.
XX	Sequence 8 AA;	CC	PT residues.
SQ		CC	CC neovascularisation or lymphangiogenesis.
Query Match	Score 42; DB 4; Length 8;	CC	CC neovascularisation or lymphangiogenesis.
Best Local Similarity	Pred. No. 1.4e-06;	CC	CC neovascularisation or lymphangiogenesis.
Matches	Mismatches 6; Conservative 2; Indels 0; Gaps 0;	CC	CC neovascularisation or lymphangiogenesis.
Qy	1 CNEESLIC 8	CC	CC neovascularisation or lymphangiogenesis.
Db	1 CNEESVVC 8	CC	CC neovascularisation or lymphangiogenesis.
SQ	Sequence 8 AA;	CC	CC neovascularisation or lymphangiogenesis.
Query Match	Score 41; DB 4; Length 8;	CC	CC neovascularisation or lymphangiogenesis.
Best Local Similarity	Pred. No. 1.4e+06;	CC	CC neovascularisation or lymphangiogenesis.
Matches	Mismatches 6; Conservative 2; Indels 0; Gaps 0;	CC	CC neovascularisation or lymphangiogenesis.
Qy	1 CNEESLIC 8	CC	CC neovascularisation or lymphangiogenesis.
Db	1 CNDESLIC 8	CC	CC neovascularisation or lymphangiogenesis.
RESULT 4		CC	CC neovascularisation or lymphangiogenesis.
AAU04538		CC	CC neovascularisation or lymphangiogenesis.
ID	AAU04538 standard; peptide; 8 AA.	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
AC	AAU04538;	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
DT	26-SEP-2001 (first entry)	CC	CC neovascularisation or lymphangiogenesis.
XX	VEGF based monocyclic peptide 16.	CC	CC neovascularisation or lymphangiogenesis.
DE		CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
KW	Human; VEGF; vascular endothelial growth factor; angiogenesis;	CC	CC neovascularisation or lymphangiogenesis.
KW	neovascularisation; lymphangiogenesis; psoriasis; tumour;	CC	CC neovascularisation or lymphangiogenesis.
KW	diabetic retinopathy; chronic inflammation; cyclical.	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
OS		CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
FH	Key Qualifiers	CC	CC neovascularisation or lymphangiogenesis.
FT	Disulfide-bond	CC	CC neovascularisation or lymphangiogenesis.
FT	1..8 /note= "This bond cyclises the peptide"	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
RESULT 5		CC	CC neovascularisation or lymphangiogenesis.
AAU04540		CC	CC neovascularisation or lymphangiogenesis.
ID	AAU04540 standard; peptide; 8 AA.	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
AC	AAU04540;	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
DT	26-SEP-2001 (first entry)	CC	CC neovascularisation or lymphangiogenesis.
XX	VEGF based monocyclic peptide 18.	CC	CC neovascularisation or lymphangiogenesis.
XX		CC	CC neovascularisation or lymphangiogenesis.
KW	Human; VEGF; vascular endothelial growth factor; angiogenesis;	CC	CC neovascularisation or lymphangiogenesis.
KW	neovascularisation; lymphangiogenesis; psoriasis; tumour;	CC	CC neovascularisation or lymphangiogenesis.
KW		CC	CC neovascularisation or lymphangiogenesis.

Sequence 8 AA:	Score	Match	DB 4;	Length	8;
SQ	84.8%	Score 39;	DB 4;	Length 8;	0;
Best Local Similarity	75.0%	Pred. No.	1.e+06;		
Matches	6	1:	Missmatches	1:	Indels
					0:
					Gaps

RESULT 7
AAV54526 standard; peptide; 8 AA.
ID AAV54526

XX	AAY54526;
AC	
XX	
DT	25-APR-2000 (first entry)
XX	
DE	Human CD4 protein target antigenic peptide p1615.
XX	Human; CD4 protein; antigenic peptide; CDR2-like sivncvrcia formation; human immune deficiency virus
KW	

XX SQ Sequence 8 AA;
 Query Match 56.5%; Score 26; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CNEESL 6
 ||||:
 Db 3 CNESSM 8

XX AC AAU08451;
 XX DT 21-NOV-2001 (first entry)
 XX Peptide A6 encoded by human VEGF-A forward primer A6-F.
 XX Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
 KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
 KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
 KW primer; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200162942-A2.
 XX PD 30-AUG-2001.
 XX PF 26-FEB-2001; 2001WO-US006113.
 XX PR 25-FEB-2000; 2000US-0185205P.
 XX PR 18-MAY-2000; 2000US-0205331P.
 XX (LUDWIG INST CANCER RES.
 PA (LICCN) LICENTIA OY.
 PA XX Polypeptides that bind cellular receptors for vascular endothelial growth
 PT factors, polynucleotides encoding them.
 PI Alicalo K, Jeltsch MM;
 XX DR WPI: 2001-516640/59.
 PS N PDB; AAS12807.
 XX Claim 9; Fig 7C: 261pp; English.
 XX The present invention relates to polypeptides that bind cellular
 PT factors, polynucleotides that bind cellular receptors for vascular endothelial growth
 CC factors that bind cellular receptors for vascular endothelial growth factors (VEGFs), the
 CC polynucleotides encoding them, and their use for identifying agents that
 CC modulate interactions between VEGFs and their receptors. VEGFs and their
 CC receptors play an important role in vasculogenesis, the development of
 CC the embryonic vasculature from early differentiating endothelial cells
 CC and angiogenesis, the process of forming new blood vessels from pre-
 CC existing ones. Modulators of interactions between VEGF and its receptors
 CC may be used to treat dysfunction of the endothelial cell regulatory
 CC system. Such disorders include cancers, abnormal angiogenesis,
 CC proliferative retinopathies, age-related macular degeneration, rheumatoid
 CC arthritis and psoriasis. The polypeptides of the invention exhibit unique
 CC receptor binding profiles compared to known naturally occurring VEGFs.
 CC AAU08445-AAU08454 represent the peptides A1-A9 which are encoded by human
 CC VEGF-A forward primers used in the methods of the present invention
 XX Sequence 8 AA;
 SQ Query Match 56.5%; Score 26; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CNEESL 6
 ||||:
 Db 3 CNDEGL 8

RESULT 1.2
 AAR80365
 ID AAR80365 standard; peptide; 8 AA.
 XX
 AC AAR80365;
 XX DT 19-APR-1996 (first entry)
 XX DE Protein polymeric adhesion substrate glutamine donor peptide #15.

XX SQ Sequence 8 AA;
 Query Match 56.5%; Score 26; DB 3; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.e+06;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CNERSLIC 8
 |||:
 Db 1 CNQQQFFC 8

RESULT 11
 AAU08451
 ID AAU08451 standard; peptide; 8 AA.

XX		XX	PI	Cappello J;
KW	pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; biocompatible material; structural integrity;	XX	XX	
KW	medical adhesive; wound closure; tissue repair; transglutaminase;	DR	WPI; 1998-387091/33.	
XX	protein polymer adhesive substrate.	XX		
OS	Synthetic.	PT	New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives.	
XX	WO9523611-A1.	PT	PT	
XX	08-SEP-1995.	PT	PT	
XX	03-MAR-1995; 95WO-US002728.	PS	Example 9; Col 49; 70pp; English.	
PF	03-MAR-1994; 94US-00205518.	XX	This is an example of a glutamine donor peptide that can be utilised in novel recombinant protein polymers of the invention. Such polymers (see AAW49710-2B) typically comprise a repetitive amino acid backbone of repetitive units having a collagen, fibron, elastin or keratin motif and at least 2 enzyme recognition sequences comprising a glutamine and/or lysine capable of enzyme catalysed isopeptide formation. The polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. They can be used as medical adhesives and sealants, in the closure of wounds and repair of damaged tissues, prostheses coatings, drug depots, CC and matrices for the transplantation of cells. (Updated on 25-MAR-2003 to correct PF field.)	
PR	(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.	XX		
PA	Pi Cappello J;	XX		
XX	DR; 1995-320413/41.	XX		
PT	Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair.	SQ	Sequence 8 AA;	
PT	XX	Query Match 54.3%; Score 25; DB 2; Length 8;		
PT	XX	Best Local Similarity 37.5%; Pred. No. 1.4e+06;		
PT	XX	Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
XX	XX	Qy 1 CNEESLIC 8		
PS	XX	Db 1 CGQSKVIC 8		
XX	XX	RESULT 14 AAY48644 standard; peptide; 8 AA.		
XX	XX	ID AAY48644		
XX	XX	AC AAY48644;		
XX	XX	AC		
CC	The peptides AAR80351-70 are examples of glutamine donor peptides which can be used to generate protein polymeric adhesion substrate (PPAS) contg. repeats of non-fibrin cross-linking donor peptide sequences (see AAR80345-10 for examples of PPAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair	XX		
CC	XX	Sequence 8 AA;		
CC	XX	Query Match 54.3%; Score 25; DB 2; Length 8;		
CC	XX	Best Local Similarity 37.5%; Pred. No. 1.4e+06;		
CC	XX	Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
CC	XX	DE Membrane dipeptidase-binding lung homing peptide #15.		
CC	XX	XX		
CC	XX	Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.		
CC	XX	XX		
CC	XX	DE Membrane dipeptidase-binding lung homing peptide #15.		
CC	XX	XX		
CC	XX	DE Synthetic.		
CC	XX	OS Homo sapiens.		
AC	XX	AC		
AC	XX	PN WO9946284-A2.		
XX	XX	DT 20-MAR-2003 (revised)		
DT	XX	DT 10-DEC-1999 (first entry)		
DT	XX	DE 16-SEP-1999.		
DT	XX	XX		
DT	XX	DE 10-MAR-1999;		
DT	XX	XX		
DE	XX	DE Glutamine donor peptide.		
XX	XX	XX		
XX	XX	DE Protein polymer; adhesive sealant; wound healing; cross-linking.		
XX	XX	XX		
OS	XX	OS Synthetic.		
OS	XX	PA (BURN-) BURNHAM INST.		
XX	XX	XX		
PN	XX	PA Rajotte D, Pasqualini R, Ruoslahti EI;		
PN	XX	XX		
PD	XX	DR WPI; 1999-571717/48.		
PD	XX	XX		
XX	XX	PT New Peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological conditions.		
PF	XX	PT		
PF	XX	XX		
PR	XX	PR 13-MAR-1998;		
PR	XX	PR 26-FEB-1999;		
PR	XX	XX		
XX	XX	XX		
PA	XX	PA (BURN-) BURNHAM INST.		
PA	XX	XX		
PN	XX	PA Rajotte D, Pasqualini R, Ruoslahti EI;		
PN	XX	XX		
PD	XX	DR WPI; 1999-571717/48.		
PD	XX	XX		
XX	XX	PT New Peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological conditions.		
XX	XX	PT		
XX	XX	XX		
PS	XX	PS Example 6; Page 144; 193pp; English.		
PS	XX	XX		
PA	XX	PA		

The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAV448618 to AAY44066 represent sequences which are used in the exemplification of the present invention. (Updated on 20-MAR-2003 to correct PR field.)

Sequence 8 AA;	
QY	Query Match 54.3%; Best Local Similarity 50.0%; Matches 4; Conservative
Dbb	Score 25; DB 2; Length 8; Pred. No. 1.4e+06; 1; Mismatches 3; Indels 0;
	CNESSLIC 8 : CGNTRLIC 8

RESULT 15	
ABG35021	ABG35021 standard; peptide; 8 AA.
XX	
AC	ABG35021;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Endostatin targeting peptide #20.
XX	
KW	Targeting peptide; cancer; Hodgkin
KW	immunosuppressive; anti-inflammatory
KW	antiatherosclerotic; antidiabetic;
KW	inflammatory disease; arthritis; a
KW	autoimmune disease; bacterium; a
XX	

XX WO200220722-A2.
XX PN
XX PD 14-MAR-2002.
XX PP 07-SEP-2001; 2001WO-US027702.
XX PR 08-SEP-2000; 2000US-0231266P.
XX PR 17-JAN-2001; 2001US-0076101.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Arap W., Pasqualini R.;
XX

XX WPI; 2002-383050/4.
XX Identifying targeting peptides useful for treating e.g. diabetes
XX mellitus, inflammatory diseases, cancer, or autoimmune diseases,
XX comprises exposing a sample to a phage display library and recovering
XX phage bound to the sample.

XX Claim 56; Page 242; 298pp; English.

XX This invention relates to a novel method for identifying disease
XX targeting peptides. The method comprises exposing a sample from an organ,
XX tissue or cell type of interest, to a phage display library and
XX recovering phage bound to the sample (the phage expresses targeting
XX peptides). The peptides identified by the method of the invention may
XX have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
XX antilatherosclerotic, antidiabetic, antibacterial and antiviral
XX activities. The methods and composition are useful for identifying
XX targeting peptides and one or more receptors for a targeting peptide. These
XX targeting peptides are used for selective delivery of therapeutic agents,
XX including gene therapy vectors and fusion proteins to specific organs,
XX tissues, or cell types in subject. The targeting peptide may also be used

for treating diseases such as diabetes mellitus, inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodgkin's disease. The present sequence represents a targeting peptide of the invention.

QY 1 CNEESLIC 8
| : | : |
Db 1 CSRSSFLC 8

Search completed: September 5, 2004, 10:38:28
Job time : 65 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:38:54 ; Search time 67 Seconds

(without alignments) 37.620 Million cell updates/sec

Title: US-09-761-636A-6
 Perfect score: 46

Sequence: 1 CNBESLIC 8

Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters:

68225

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 100%

Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:*

```

1: /cgn2_6/prodata/2/pubpa/US07_PUBCOMB_pep:*
2: /cgn2_6/prodata/2/pubpa/FCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpa/US06_NEWPUB.pep:*
4: /cgn2_6/prodata/2/pubpa/US07_NW_PUBCOMB_pep:*
5: /cgn2_6/prodata/2/pubpa/US08_PUBCOMB_pep:*
6: /cgn2_6/prodata/2/pubpa/US09_NEWPUB.pep:*
7: /cgn2_6/prodata/2/pubpa/US10_PUBCOMB_pep:*
8: /cgn2_6/prodata/2/pubpa/US08_NEWPUB.pep:*
9: /cgn2_6/prodata/2/pubpa/US09_NEWPUBCOMB_pep:*
10: /cgn2_6/prodata/2/pubpa/US08_PUBCOMB_pep:*
11: /cgn2_6/prodata/2/pubpa/US09_PUBCOMB_pep:*
12: /cgn2_6/prodata/2/pubpa/US09_NEWPUB.pep:*
13: /cgn2_6/prodata/2/pubpa/US10_PUBCOMB_pep:*
14: /cgn2_6/prodata/2/pubpa/US10_PUBCOMB_pep:*
15: /cgn2_6/prodata/2/pubpa/US10_PUBCOMB_pep:*
16: /cgn2_6/prodata/2/pubpa/US10_NEWPUB_pep:*
17: /cgn2_6/prodata/2/pubpa/US60_NEWPUBCOMB_pep:*
18: /cgn2_6/prodata/2/pubpa/US60_PUBCOMB_pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	SEQ ID NO	LENGTH: 8	TYPE: PRT	ORGANISM: Homo sapiens
<hr/>									
1	46	100.0	8	9	US-09-761-636A-6	US-09-761-636A-6	Sequence 6, Appli	1 CNEESLIC 8	RESULT 1
2	43	93.5	8	9	US-09-761-636A-20	Sequence 20, Appli	Sequence 20, Appli		US-09-761-636A-20
3	42	91.3	8	9	US-09-761-636A-22	Sequence 22, Appli	Sequence 22, Appli	1 CNEESLIC 8	Query Match
4	41	89.1	8	9	US-09-761-636A-19	Sequence 19, Appli	Sequence 19, Appli	100.0%; Score 46; DB 9; Length 8;	Best Local Similarity 100.0%; Pred. No. 1.2e+06;
5	39	84.8	8	9	US-09-761-636A-19	Sequence 21, Appli	Sequence 21, Appli	0; Mismatches 0; Indels 0; Gaps 0;	Matches 8; Conservative
6	26	55.5	8	9	US-09-795-006A-133	Sequence 133, App	Sequence 133, App		Sequence 14, Appli
7	25	54.3	8	12	US-10-363-208-108	Sequence 108, App	Sequence 108, App		Sequence 25, Appli
8	24	52.2	8	9	US-09-795-006A-142	Sequence 142, App	Sequence 142, App		Sequence 115, App
9	23	50.0	8	9	US-09-840-277-25	Sequence 14, Appli	Sequence 14, Appli		Sequence 115, App
10	23	50.0	8	9	US-09-185-008-115	Sequence 25, Appli	Sequence 25, Appli		Sequence 457, App
11	23	50.0	8	12	US-10-609-217-57	Sequence 457, App	Sequence 457, App		Sequence 457, App
12	23	50.0	8	12	US-10-363-208-74	Sequence 74, Appli	Sequence 74, Appli		Sequence 82, Appli
13	23	50.0	8	12	US-10-363-208-82	Sequence 82, Appli	Sequence 82, Appli		Sequence 457, App
14	23	50.0	8	12	US-10-632-388-457	Sequence 457, App	Sequence 457, App		
15	23	50.0	8	12	US-10-632-388-457	Sequence 457, App	Sequence 457, App		

ALIGNMENTS

SEQ ID NO 6

Description

SOFTWARE: PatentIn version 3.0

```

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 106448505 Achen et al
; CURRENT APPLICATION NUMBER: US 09/761,636A
; PRIORITY FILING DATE: 2001-01-18
; PRIORITY NUMBER: US 60,176,293
; PRIORITY NUMBER: US 60,204,590
; PRIORITY FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

```

```

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 106448505 Achen et al
; CURRENT APPLICATION NUMBER: US 09/761,636A
; PRIORITY FILING DATE: 2001-01-18
; PRIORITY NUMBER: US 60,176,293
; PRIORITY NUMBER: US 60,204,590
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

```

```

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIORITY FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
SEQ ID NO: 20
LENGTH: 8
TYPE: PRT
ORGANISM: synthetic construct
US-09-761-636A-20

Query Match Score 93.5%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Exact 0; Insertions 0; Deletions 0;

RESULT 3
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIORITY FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
SEQ ID NO: 22
LENGTH: 8
TYPE: PRT
ORGANISM: synthetic construct
US-09-761-636A-22

Query Match Score 91.3%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Exact 0; Insertions 0; Deletions 0;

RESULT 4
US-09-761-636A-19
; Sequence 19, Application US/09761636A
; Patent No. US20020065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
Qy 1 CNEBSLIC 8
Db 1 CNEBSVNC 8

Query Match Score 84.8%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Exact 0; Insertions 0; Deletions 0;

RESULT 6
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
GENERAL INFORMATION:
; APPLICANT: Alitalo, et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/359/7B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIORITY FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR APPLICATION NUMBER: US 60/185,205
Qy 1 CNEBSLIC 8
Db 1 CNEBSFIC 8

Query Match Score 84.8%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Exact 0; Insertions 0; Deletions 0;

RESULT 7
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
GENERAL INFORMATION:
; APPLICANT: Alitalo, et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/359/7B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIORITY FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR APPLICATION NUMBER: US 60/185,205
Qy 1 CNEBSLIC 8
Db 1 CNEBSFIC 8

```



```

; PRIORITY FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
; US-09-840-277-25

Query Match      50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
Db   1 CWDDGLMC 8

RESULT 13
US-10-609-217-457
; Sequence 74, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774_P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 74
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1) .(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-74

Query Match      50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
Db   1 CRASAMVC 8

RESULT 14
US-10-363-208-82
; Sequence 82, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774_P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1) .(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-82

Query Match      50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
Db   1 CRTSSYVC 8

RESULT 15
US-10-609-217-457
; Sequence 457, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHI-JAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 113
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
; US-10-609-217-457

Query Match      50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

Qy 1 CNEESLIC 8
 Db 1 CRASAMVC 8

RESULT 15
 US-10-632-388-457
 ; Sequence 457, Application US/10632388
 ; Publication No. US20040053845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: LIU, CHUAN FA
 ; APPLICANT: CHEETHAM, JANET C.
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527
 ; CURRENT APPLICATION NUMBER: US/10/632,388
 ; CURRENT FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US/09/428,082B
 ; PRIOR FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 1133
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 457
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
 US-10-632-388-457

Query Match 50.0%; Score 23; DB 12; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CNEESLIC 8
 Db 1 CWDDGLMC 8

Search completed: September 5, 2004, 10:44:41
 Job time : 67 secs

This page blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	28	22	47.8	8	3	US-09-258-754-256
OM protein - protein search, using sw model		29	22	47.8	8	3	US-09-042-107-36
Run on: September 5, 2004, 10:37:23 ; Search time 20 Seconds	20.650 Million cell updates/sec	30	22	47.8	8	3	US-09-042-107-48
Title: US-09-761-636A-6	(without alignments)	31	22	47.8	8	3	US-09-042-107-256
Perfect score: 46		32	22	47.8	8	4	US-09-087-859-1071
Sequence: 1 CNEBSSLIC 8		33	22	47.8	8	4	US-09-187-859-3624
Scoring table: BLOSUM62		34	22	47.8	8	4	US-09-187-859-3664
Gapext: 0.5		35	22	47.8	8	4	US-09-039-542B-3624
Searched: 389414 seqs, 51625971 residues		36	22	47.8	8	4	US-09-072-250D-36
Total number of hits satisfying chosen parameters:	71086	37	22	47.8	8	4	US-09-022-250D-48
Minimum DB seq length: 0		38	22	47.8	8	4	US-09-022-250D-256
Maximum DB seq length: 8		39	22	47.8	8	4	US-09-046-423-11
Post-processing: Minimum Match 0% Maximum Match 100%		40	21	45.7	5	4	US-09-087-859-3663
Listing first 45 summaries		41	21	45.7	5	4	US-09-039-542B-3663
Database : Issued Patents AA:*		42	21	45.7	6	4	US-09-187-859-985
1: /cggn2_6/prodata/2/iaa/5A_COMB.pep:*		43	21	45.7	6	4	US-09-187-859-2242
2: /cggn2_6/prodata/2/iaa/5B_COMB.pep:*		44	21	45.7	6	4	US-09-039-542B-285
3: /cggn2_6/prodata/2/iaa/6A_COMB.pep:*		45	21	45.7	6	4	US-09-039-542B-2242
4: /cggn2_6/prodata/2/iaa/6B_COMB.pep:*							
5: /cggn2_6/prodata/2/iaa/PCUTS_COMB.pep:*							
6: /cggn2_6/prodata/2/iaa/backfiles1.dep:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
RESULTS							
RESULT 1							
US-09-100-409A-27							
; Sequence 27, Application US/09100409A							
; Patent No. 6090398							
; GENERAL INFORMATION:							
; APPLICANT: Wang, Chang Y.							
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR PREVENTION AND TREATMENT OF HIV INFECTION AND							
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND							
; NUMBER OF SEQUENCES: 64							
; CORRESPONDENCE ADDRESS:							
; ADDRESS: MORGAN & FINNEGANS							
; STREET: 345 Park Avenue							
; CITY: New York							
; STATE: NY							
; COUNTRY: USA							
; ZIP: 10154-0054							
COMPUTER READABLE FORM:							
MEDIUM TYPE: Floppy disk							
COMPUTER: IBM PC compatible							
OPERATING SYSTEM: PC-DOS/MS-DOS							
SOFTWARE: PatentIn Release #1.0, Version							
SOFTWARE: #1.25							
CURRENT APPLICATION DATA:							
APPLICATION NUMBER: US/09/100,409A							
FILING DATE:							
CLASSIFICATION: 514							
ATTORNEY/AGENT INFORMATION:							
NAME:							
REGISTRATION NUMBER:							
SEQUENCE CHARACTERISTICS:							
LENGTH: 8 amino acids							
TYPE: amino acid							
TOPOLOGY: linear							
MOLECULE TYPE: Peptide							
US-09-100-409A-27							
Query Match							
Best Local Similarity							
Matches 4; Conservative							
Score 30; DB 3; Length 8;							
Pred. No. 3e-05; 2; Mismatches 0; Indels 0;							
Qy 1 CNBSSLIC 8							
Db 1 CNQSSFLC 8							

RESULT 2
 US-09-089-878-3
 Sequence 3, Application US/09089878
 Patent No. 6458528
 GENERAL INFORMATION:
 APPLICANT: Groat, Randall G.
 APPLICANT: O'Connor, Thomas P.
 APPLICANT: Mermier, Brion
 TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
 TITLE OF INVENTION: USING ENV/GAG POLYPEPTIDE MARKERS
 FILE REFERENCE: 00088/111001
 CURRENT APPLICATION NUMBER: US/09/089-878
 CURRENT FILING DATE: 1998-06-03
 EARLIER APPLICATION NUMBER: US 60/085,615
 EARLIER FILING DATE: 1998-05-15
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Feline immunodeficiency virus
 US-09-089-878-3

Query Match Score 56.5%; Best Local Similarity 37.5%; Matches 3; Conservati 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
 Db 1 CQGSKVIC 8

RESULT 4
 US-09-258-754-49
 Sequence 49, Application US/09258754
 Patent No. 6174687
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 APPLICANT: Pasqualini, Renata
 APPLICANT: Rajtter, Daniel
 TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using Peptides
 FILE REFERENCE: P-LJ 3443
 CURRENT APPLICATION NUMBER: US/09/258,754
 CURRENT FILING DATE: 1999-02-26
 EARLIER APPLICATION NUMBER: 09/042,107
 EARLIER FILING DATE: 1998-03-13
 NUMBER OF SEQ ID NOS: 452
 SEQ ID NO 49
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-258-754-49

Query Match Score 54.3%; Best Local Similarity 50.0%; Matches 4; Conservati 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
 Db 1 CGNETLRC 8

RESULT 5
 US-09-042-107-49
 Sequence 49, Application US/09042107
 Patent No. 623287
 GENERAL INFORMATION:
 APPLICANT: Pasqualini, Renata
 TITLE OF INVENTION: Molecules that Home to Various Selected Organs or Tissues
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLIER, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/397,633A
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20,015
 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277239
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match Score 54.3%; Best Local Similarity 50.0%; Matches 4; Conservati 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
 Db 1 :|:|

Db 1 CGNETLRC 8

RESULT 6

US-09-722-250D-49

Sequence 49, Application US/09722250D

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or Tissues

FILE REFERENCE: P-LJ 4514

CURRENT APPLICATION NUMBER: US/09/722,250D

CURRENT FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: US 09/042,107

PRIOR FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 437

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 49

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-722-250D-49

RESULT 7

US-08-973-551-14

Sequence 14, Application US/08973551

GENERAL INFORMATION:

Patent No. 6113902

APPLICANT: Chermann, Jean-Claude

APPLICANT: Le Conte, Carole

APPLICANT: Galea, Pascale

TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF DIAGNOSIS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

STATE: D.C.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,551

FILING DATE: 30-DEC-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/01006

FILING DATE: 28-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95-07914

FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Granados, Patricia D.

REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 65691/130

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-973-551-14

Query Match 50.0%; Score 23; DB 3; Length 7;

Best Local Similarity 80.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEES 5
| | | |
Db 2 CNPES 6

RESULT 8

US-08-520-535-3

Sequence 3, Application US/08520535

GENERAL INFORMATION:

Patent No. 5817750

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,535

FILING DATE: 28-AUG-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Kathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 1794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: circular

US-08-520-535-3

Query Match 50.0%; Score 23; DB 2; Length 8;

Best Local Similarity 37.5%; Pred. No. 3e+05;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEE\$LC 8
| : |
Db 1 CWDGGLMC 8

RESULT 9

```

US-09-258-754-33

Query Match      50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05; 4; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CNEEESLIC 8
Db      1 CRHESSSC 8

RESULT 11
US-09-258-754-42
; Sequence 42, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
;   APPLICANT: Ruoslahti, Erkki
;   APPLICANT: Pasqualini, Renata
;   APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
;   Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-258-754-42

Query Match      50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05; 3; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CNEEESLIC 8
Db      1 CHEGYLTC 8

RESULT 12
US-09-258-754-214
; Sequence 214, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
;   APPLICANT: Ruoslahti, Erkki
;   APPLICANT: Pasqualini, Renata
;   APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
;   Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-258-754-214

Query Match      50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05; 2; Mismatches 3; Indels 0; Gaps 0;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1 CNEBSLIC 8
 Db 1 CFKSTLIC 8

RESULT 13
 US-09-042-107-33
 ; Sequence 33, Application US/09042107
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
 ; TITLE OF INVENTION: Tissues
 ; FILE REFERENCE: P-LJ 2892
 ; CURRENT APPLICATION NUMBER: US/09/042,107
 ; CURRENT FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 436
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-042-107-214

Query Match 50.0%; Score 23; DB 3; Length 8;
 Best Local Similarity 37.5%; Pred. No. 3e+05;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEBSLIC 8
 Db 1 CFKSTLIC 8

Search completed: September 5, 2004, 10:40:46
 Job time : 20 secs

Query Match 50.0%; Score 23; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CNEBSLIC 8
 Db 1 CRHESSSC 8

RESULT 14
 US-09-042-107-42
 ; Sequence 42, Application US/09042107
 ; Patent No. 6232287
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
 ; TITLE OF INVENTION: Tissues
 ; FILE REFERENCE: P-LJ 2892
 ; CURRENT APPLICATION NUMBER: US/09/042,107
 ; CURRENT FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 436
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-042-107-42

Query Match 50.0%; Score 23; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CNEBSLIC 8
 Db 1 CHEGYLTC 8

RESULT 15
 US-09-042-107-214
 ; Sequence 214, Application US/09042107
 ; Patent No. 6232287
 ; GENERAL INFORMATION:

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:44:49 ; Search time 22 Seconds

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 C1SVPPLTSPVC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : PIR 78-*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	36.1	11	D57789	Gallbladder stone
2	20	32.8	6	2	MHC H2-L antigen -
3	19	31.1	5	165546	glycogen phosphorylase
4	18	29.5	10	2	hypothetical prote
5	17	27.9	8	C39191	hypothetical prote
6	17	27.9	10	C39111	205K exoantigen -
7	17	27.9	10	2	Ig heavy chain C r
8	17	27.9	11	PR0944	T-cell receptor be
9	17	27.9	11	2	gamma-interferon-i
10	16	26.2	4	PH0929	T-cell receptor be
11	16	26.2	9	151049	metallothionein-A
12	16	26.2	9	A60356	118K stomach cance
13	16	26.2	9	PT0247	Ig heavy chain CRD
14	16	26.2	10	2	polyalacturonase
15	16	26.2	10	A61622	vitellogenin, 190k
16	16	26.2	10	PH0926	T-cell receptor be
17	16	26.2	10	A32195	Na+/K+-exchanging
18	16	26.2	11	BCLQ2M	tachykinin II - mi
19	15	24.6	11	S00616	paraporal crystal
20	15	24.6	10	2	peptide-N-(N-acet
21	15	24.6	11	BN0042	IG H chain V-D-J r
22	15	24.6	11	PH0941	stamin - mouse
23	14	23.0	5	E60274	T-cell receptor be
24	14	23.0	6	A35039	major protein anti
25	14	23.0	7	EC1316	hypothetical colla
26	14	23.0	8	S08996	large granule 13 c
27	14	23.0	8	B49823	hypertrehalosemic
28	14	23.0	8	B44960	adipokinetic hormo
29	14	23.0	8	A33995	neuropeptide Led-C
					adipokinetic hormo

RESULT 1
D57789
gallbladder stone matrix protein, 14.5K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C;Accession: D57789
R;Binette, J.-P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Reference number: A57789

A;Status: Preliminary

A;Molecule type: protein

A;Residues: 1-11 NN>

Query Match 36.1%; Score 22; DB 2; Length 11;

Best Local Similarity 66.7%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 5 PLTSVP 10
Db 1 PATSAP 6

RESULT 2

MHC H2-L antigen - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C;Accession: I65546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.

Cell 44, 261-272, 1986

A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and thei

A;Reference number: I52778; PMID:86106202; PMID:510743

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-6 <RRS>

Cross-references: GB:M12483; NID:g199565; PID:AAA19663..1; PMID:g554234

Query Match 32.8%; Score 20; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 9 VPC 11
Db 2 VPC 4

RESULT 3
A60321
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N;Alternate names: glycogen phosphorylase b
C;Species: Liiza ramata
C;Accession: A60521
R;Bonansea, L.; Bonanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A;Reference number: A60521; MUID:90227907; PMID:2109669
A;Molecule type: Protein
A;Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ISVP 5
Db 2 ISVP 5

RESULT 4
C39111
Hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Accession: C39111
R;peer, B.S.; Bedzyk, L.; salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A;Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A;Reference number: A39191; MUID:91100280; PMID:1844135
A;Accession: C39191
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <SPE>
A;Cross References: GB:MB37699

Query Match Score 18; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 3 SVPIITSV 9
Db 4 SRPWTSI 10

RESULT 5
G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Accession: G33098
R;Nichols, J.H.; Hager, L.P.
Submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Status: preliminary
A;Molecule type: Protein
A;Residues: 1-8 <NIC>

Query Match Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 VPLTSV 9
Db 2 VPLXLV 7

RESULT 6

C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stoutii (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: C39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (*Eptatretus stoutii*) exhibits structural similarity to the Ig heavy chain C region
A;Reference number: A39111; MUID:9115668; PMID:2000382
A;Accession: C39111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAR>
C;Keywords: heterotetramer;

Query Match Score 17; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ISVP 6
Db 4 ISSPL 8

RESULT 7
PH0944
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0944
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0891
A;Molecule type: mRNA
A;Residues: 1-10 <GOI>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon GAC for residue 9 as Glu
C;Keywords: T-cell receptor

Query Match Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CIVP 5
Db 1 CASSP 5

RESULT 8
S21727
Gamma-interferon-induced protein IP-10 precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S21727
R;Wei, M.L.; Creswell, P.
Nature 356, 443-446, 1992
A;Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-
A;Reference number: S21727; MUID:1557127
A;Accession: S21727
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <WEI>
Query Match Score 17; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ISVPITSV 9
Db 3 LDVPTAAV 10

RESULT 9
 PH0929 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0929 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1475, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0929
 A;Molecule type: mRNA
 A;Residues: 1-11 <GOL>
 A;Experimental source: concanavalin A-activated lymphoblast
 C;Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

Qy 1 C1SVPLT 7
 Db 1 CASRPGT 7

RESULT 10
 151049 metallothionein-A - rainbow trout (fragment)
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Accession: T1049 R;Olsson, P.E.; Kling, P.; Ertell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
 A;Title: Structural and functional analysis of the rainbow trout (*Oncorhynchus mykiss*) me
 A;Reference number: 151049; MUID:93324545; PMID:7601121
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-4 <OUL>
 A;Cross-references: EMBL:X80181; NID:91019799; PIDN:CAA56466.1; PID:94379328

Query Match 26.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 PC 11
 Db 3 PC 4

RESULT 11
 A60356 118K stomach cancer antigen - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
 C;Accession: A60356 R;Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
 A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
 A;Accession: A60356
 A;Molecule type: protein
 A;Residues: 1-9 <SHI>
 C;Keywords: glycoprotein

Query Match 26.2%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2;
 Indels 0; Gaps 0;

Qy 4 VPRLTSV 9
 Db 1 IPLKPV 6

RESULT 12
 PH0247 Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0247 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
 A;Reference number: PT0222; MUID:9110833; PMID:1899102
 A;Accession: PT0247
 A;Molecule type: DNA
 A;Residues: 1-9 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 26.2%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2;
 Indels 0; Gaps 0;

Qy 3 SVPLTS 8
 Db 2 SAPIDS 7

RESULT 13
 S62880 polygalacturonase (EC 3.2.1.15) IV - *Aspergillus* sp. (fragment)
 C;Species: *Aspergillus* sp.
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C;Accession: S62880 R;Stratilova, E.; Dzurova, M.; Markovic, O.; Joeinwall, H.
FEBS Lett. 382, 164-166, 1996
 A;Title: An essential tyrosine residue of *Aspergillus* polygalacturonase.
 A;Reference number: S62880; PMID:9619656; PMID:8612742
 A;Molecule type: protein
 A;Residues: 1-10 <STR>
 C;Keywords: glycosidase; hydrolase
 F;Active site: Tyr #scatrus predicted

Query Match 26.2%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 2; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 PC 11
 Db 9 PC 10

RESULT 14
 A61622 vitellogenin, 190k chain - gypsy moth (fragment)
 N;Contains: vitellogenin, 190k chain - gypsy moth
 C;Species: *Lymantria dispar* (gypsy moth)
 C;Accession: A61622 R;Hiremath, S.; Ebhita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
 A;Title: Purification and characterization of vitellogenin from the gypsy moth, *Lymantri*
 A;Reference number: A61622
 A;Accession: A61622
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <HIR>
 C;Keywords: egg yolk; hemolymph

Query Match 26.2%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 5 PLT 7
Db 2 PLT 4

RESULT 15
PH0926
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0926
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J;Exp. Med.: 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PMID:92078857; PMID:1836012
A;Accession: PH0926
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon AGA for residue 4 as Thr
C;Keywords: T-cell receptor

Query Match 26.2% Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CIGVP 5
Db 1 CASRP 5

Search completed: September 5, 2004, 10:48:24
Job time : 23 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	23	37.7	11	TIN4_HOPTI	P82654 hoplobatrachus
2	19	31.1	11	TIN1_HOPTI	P82651 hoplobatrachus
3	18	29.5	8	COW2_CONPU	P58795 conus purpu
4	17.5	28.7	9	NGMT_BOVIN	P29177 bos taurus
5	17	27.9	10	UPA4_HUMAN	P30000 homo sapien
6	16	26.2	10	DPK1_CONMR	P58897 conus marmo
7	15	24.6	10	DPK2_LOCMI	P4188 locusta mig
8	14	23.0	8	AKH_TABAT	P14525 tabanus atr
9	14	23.0	8	HTF2_PERAM	P04549 periplaneta
10	14	23.0	8	UPAA_HUMAN	P30046 homo sapien
11	14	23.0	9	DNF1_LOCMI	P16339 locusta mig
12	14	23.0	9	YBF1_AZOVIA	P25825 azotobacter
13	14	23.0	10	BPP2_BOTIN	P01022 bothrops ja
14	14	23.0	10	HTF2_CARMO	P11335 carausius m
15	14	23.0	10	HTF TABAT	P14596 tabanus atr
16	14	23.0	11	BPP3_BOTIN	P3043 bothrops in
17	14	23.0	11	BPP4_BOTIN	P30124 bothrops in
18	14	23.0	11	EPQB_AKGHA	P01021 agkistrodon
19	14	23.0	11	PQQC_PSEFL	P55173 pseudomonas
20	13	21.3	6	E101_LITRU	P82096 litoria rub
21	13	21.3	8	UPA1_HUMAN	P30087 homo sapien
22	13	21.3	9	CONO_CONST	P05467 conus striata
23	13	21.3	10	BPP2_BOTIN	P30122 bothrops in
24	13	21.3	10	BPV_VIPMAS	P3151 viper aspis
25	13	21.3	10	COXH_ONCMY	P8031 oncorthynchus
26	13	21.3	10	COXQ_SHEEP	P80337 ovis aries
27	13	21.3	10	ESTA_SCHGUA	P81012 schizaphis
28	13	21.3	10	NS1_MYCTU	P8113 mycobacterium
29	12	19.7	7	TPFY_PACDA	P83455 pachymedusa
30	12	19.7	8	ALL6_CYDPO	P82157 cydia pomonella
31	12	19.7	8	FUS5_FUSSO	P8101 fusarium sojae
32	12	19.7	8	VGLG_HSV2B	P81780 herpes simplex
33	12	19.7	9	FARS5_PENMNO	P83320 penaeus monodon

ALIGNMENTS					
RESULT 1					
ID	TIN4_HOPTI	STANDARD;	PRT;	11 AA.	
AC	P82654;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DB	Tigerinin-4.				
OS	Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidea; Ranidae;				
OC	Hoplobatrachus				
NCBI_TaxID	103373;				
RN	SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.				
RP	SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.				
RC	TISSUE=Skin secretion;				
RX	Pubmed=1103127;				
RA	Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P., Devi A.S., Nagaraj R., Sitaran N.,				
RT	"Tigerinin": novel antimicrobial peptides from the Indian frog Rana tigerina."				
RT	J. Biol. Chem. 276:2701-2707(2001).				
RL	-1- FUNCTION: Antibacterial activity against <i>B. subtilis</i> , <i>E. coli</i> , <i>S. aureus</i> , <i>M. luteus</i> , <i>P. putida</i> and <i>S. cerevisiae</i> .				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- TISSUE SPECIFICITY: Skin.				
CC	-1- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.				
KW	Amphibian defense peptide; Antibiotic.				
FT	DISULFID	3	11		
SQ	SEQUENCE 11 AA: 1248 MW: 117DBEFD37605DCB CRC64;				
Query	Match Score 23; DB 1; Length 11; Best Local Similarity 50.0%; Pred. No. 1_8e+02; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;				
Db	1 CISVBL 6 : : 3 CYAIFL 8				
RESULT 2					
ID	TIN1_HOPTI	STANDARD;	PRT;	11 AA.	
AC	P82651;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DB	Tigerinin-4.				
OS	Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidea; Ranidae;				
OC	Hoplobatrachus				
NCBI_TaxID	103373;				
RN	SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.				
RC	TISSUE=Skin secretion;				

RX PubMed=11031261;
 RA Purna Sai K.; Jagannadham M.V.; Vairamani M.; Raju N.P.,
 Devi A.S.; Nagaraj R.; Sitaran N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 tigerina.",
 RT J. Biol. Chem. 276:2701-2707 (2001).
 CC :- FUNCTION: Antibacterial activity against *B. subtilis*, *E.coli*,
S. aureus, *M. luteus*, *P. putida* and *S.cerevisiae*.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Skin.
 CC -|- MASS SPECTROMETRY: MN=1342; METHOD=MALDI.
 KW AMPHIBIAN defense peptide; Antibiotic; Fungicide; Amidation.
 FT DISULFID 2 10
 PT MOD RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; A0087DC960476056 CRC64;

Query Match Score 19; DB 1; Length 11;
 Best Local Similarity 33.3%; Pred. No. 9.7e+02;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0; Gaps 1;

Qy 1 C1SVP 6
 | :|:
 Db 2 CTM1PI 7

RESULT 3
 ID_COW2_CONP STANDARD; PRT; 8 AA.
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-Contryphan P.
 OS *Conus purpurascens* (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
 Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TAXID=41690;

RN 1
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RK MEDLINE=99388839; Pubmed=10461743;
 RA Jacobson R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 PT "A novel D-leucine-containing Conus peptide: diverse conformational
 dynamics in the contryphan family.",
 RT Res. 54:93-99(1993).
 RC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- MASS SPECTROMETRY: MW=888.4; METROD=LSIMS.
 CC -|- SIMILARITY: Belongs to the contryphan family.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 8
 PT MOD RES 4 4 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A367672232CEBB CRC64;

Query Match Score 18; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Gaps 1;

Qy 1 C1SVP 5
 | :|:
 Db 2 CVLIP 6

RESULT 4
 MGMT_BOVIN STANDARD; PRT; 9 AA.
 AC P29177;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-

DB methylguanine-DNA methyltransferase) (Fragment).
 GN MGMT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 NCBI_TAXID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B.; Hall J.; Karren P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 methyltransferase.",
 RL Nucleic Acids Res. 18:17-21(1990).
 CC -|- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically
 transferring the alkyl group at the O-6 position to a cysteine
 residue in the enzyme. This is a suicide reaction: the enzyme is
 irreversibly inactivated.
 CC -|- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
 CC (protein)-L-cysteine = DNA (without 6-O-methylguanine) + protein
 CC S-methyl-L-cysteine.
 CC -|- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
 DR InterPro; IPR001497; Methyltransf_1.
 DR PROSITE; PS00374; MGNT; PARTIAL.
 KW DNA repair; Transferase; Methyltransferase.
 FT NON_TER 1 1 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 9 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match Score 17.5%; Pred. No. 1.4e+05;
 Best Local Similarity 37.5%; Pred. No. 1.4e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 1; Gaps 1; Gaps 1;

Qy 4 VPRTSVP 11
 | :|:
 Db 3 IPIR-PC 9

RESULT 5
 UBA4_HUMAN STANDARD; PRT; 10 AA.
 ID UBA4_HUMAN
 AC P30050;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93094937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -|- MISCELLANEOUS: On the 2D-gel, the determined PI of this unknown
 protein is: 4.8. Its MW is: 40.5 kDa.
 CC -|- MISCELLANEOUS: This spot is on a position thought to be that of
 Zn-alpha-2 glycoprotein, but it does not correspond to that.
 DR SWISS-2DPAGE; P30090; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 4 4
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;

Query Match	27.9%	Score 17;	DB 1;	Length 10;				
Best Local Matches	80.0% ; 4; Conservative	Prd. No. 2e+03 ; 0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	4 VPLTS B							
Db	2 VPNTS 6							
RESULT 6								
CXLI_1 CONMR	STANDARD;	PRT;	11 AA.					
ID	CXLI_1 CONMR							
AC	P58807;							
DT	28-FEB-2003 (Rel. 41; Created)							
DT	28-FEB-2003 (Rel. 41; Last sequence update)							
DT	28-FEB-2003 (Rel. 41; Last annotation update)							
DE	Lambda-conotoxin CMrVIA.							
OS	Conus marmoratus (Marble cone).							
OC	Apogastropoda; Caenogastropoda; Gastropoda; Orthogastropoda;							
OC	Neogastrropoda; Conoidea; Conidae; Conus.							
OX	NCBI_TAXID=42752;							
RN	[1]							
RP	SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.							
RC	TISSUE=Venom.							
RX	MEDLINE=20564325; PubMed=10988292;							
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,							
RA	Seow K.T., Bay B.-H.,							
RA	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of <i>Conus marmoratus</i> ."							
RT	"Lambda-conotoxins. A new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of <i>Conus marmoratus</i> ."							
RT	J. Biol. Chem. 275:39516-39522(2000).							
RL	- - FUNCTION: Inhibits the neuronal noreadrenaline transporter.							
CC	- - SUBCELLULAR LOCATION: Secreted.							
CC	- - TISSUE SPECIFICITY: Expressed by the venom duct.							
CC	- - MASS SPECTROMETRY: MW=1237.93; MW_FRR=0.21; METHOD=Electrospray.							
KW	Neurotoxin; Toxin; Hydroxylation.							
FT	DISULFID 2							
FT	DISULFID 3							
FT	MOD RES 10							
FT	MOD RES 10							
FT	HYDROXYLATION.							
SEQUENCE	11 AA;	1226 MW;	277AAC60B7232B58	CRC64;				
SQ								
Query Match	26.2%	Score 16;	DB 1;	Length 11;				
Best Local Matches	100.0% ; 2; Conservative	Prd. No. 3.e+03 ; 0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	10 PC 11							
Db	10 PC 11							
RESULT 7								
LPK2 LOCMI	STANDARD;	PRT;	10 AA.					
ID	LPK2 LOCMI							
AC	P14488;							
DT	01-NOV-1995 (Rel. 32; Created)							
DT	01-NOV-1995 (Rel. 32; Last sequence update)							
DT	28-FEB-2003 (Rel. 41; Last annotation update)							
OS	Locusta migratoria (LOM-PK-2) (FXPR1-amide).							
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Acridoidea; Acridia; Oedipodinae; Locusta.							
OC	Acridoidea; Acridia; Oedipodinae; Locusta.							
OX	NCBI_TAXID=7004;							
RN	[1]							
RP	SEQUENCE.							
RC	TISSUE-Brain;							
RX	MEDLINE=94091539; PubMed=7903606;							
RA	Schoofs L.; Holman G.M., Nachman R., Proost P., van Damme J., de Loof A.;							
RT	"Isolation, identification and synthesis of locustaspyrokinin II from <i>Locusta migratoria</i> , another member of the FXPR1-amide Peptide							
RT	13-AUG-1987 (Rel. 05, Created)							
RESULT 9								
HTF2_PERAM	STANDARD;	PRT;	8 AA.					
ID	HTF2_BERAM							
AC	P04549;							
DT	13-AUG-1987 (Rel. 05, Created)							

RESULT 10

UPA_HUMAN STANDARD; PRT: 8 AA.

ID UPAA_HUMAN
AC P30996;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 43, Last annotation update)

OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattaria orientalis (Oriental cockroach).
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Blattidae; Periplaneta; Arthropoda; Dictyoptera; Blattaria; Blattoidea;
OX NCBI_TaxID=6978;

RN [1]

RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=548658;
RA Witten J.L., Schaffner M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry";
RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).

RN [2]

RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84498179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A./
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardia of Periplaneta americana.";
RI Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).

RN [3]

RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Geede G., Kellner R.;
RT "the metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289 (1989).

RN [4]

RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90251659; PubMed=2401127;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaeemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blatta germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry";
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
CC -1- FUNCTION: Hypertrehalosaeemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the ARH / RPCH family.

DR PIR: BA4960; BA4960.
DR PIR: BA49623; BA49823.
DR InterPro: IPR02047; ARH.
DR PROSITE: PS00256; ARH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 23.0%; score 14; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

RESULT 11

DNP1_LOCMI STANDARD; PRT: 9 AA.

ID DNP1_LOCMI
AC P16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acrideromorpha;
OC Acridoidea; Acridae; Oedipodinae; Locusta.
NCBI_TaxID=7004;

RN [1]

RP SEQUENCE.
RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88070077; PubMed=3699410;
RA Proix J.-P., Miller C.A., Li J.-P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A./
RT "Identification of an arginine vasopressin-like diuretic hormone from
Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186 (1987).
CC -1- FUNCTION: DIURETIC HORMONE.
CC -1- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
CC PIR: A29477; A29477.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone; 1.
DR PROSITE: PS00264; NEUROTOPHOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation
FT DISULFID 1 IN F1.
FT DISULFID 1 INTERCHAIN (WITH C-6) (IN F2).
FT DISULFID 6 INTERCHAIN (WITH C-1) (IN F2).
MOD_RES 9 AMIDATION.

Query 6 JTSVP 10
Matches 2 LTFTP 6

DB 2 LTFTP 6

DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00255; AKH; 1.
 KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LTSVP 10
 Db 2 LTFTP 6

RESULT 15
 HTF TABAT ID - HTF TABAT STANDARD; PRT; 10 AA.
 AC PI45961; DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosaemic factor (HTOH) (Dipteran corpora cardiaca factor II)
 DE (DCC II).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 NCBI TaxID=7207;
 RN [1]

RN

RESULT 4
 DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)
 DB Transposase (Fragment).
 GN TNP17.
 OS Acinetobacter sp. BW3.
 OG Plasmid pKUH207.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Moraxellaceae; Acinetobacter.
 OC NCBI_TaxID=106395;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BW3; PLASMID=pKUH207;
 RA Khodoloi G.Y., Mindlin S.Z., Gorlenko Z.M.,
 RA Yurieva O.V., Mindlin Z.M., Gorlenko Z.M.,
 RA Nikiforov V.G.;
 RT "PKUH2-like aberrant transposons and possible mechanisms of their
 dissemination."
 RT Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RL [2]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BW3; PLASMID=pKUH207;
 RA Petrova M.A., Nikiforov V.G.;
 RT "A young family of transposable adaptive DNA segments identified in
 the Actinobacter genus."
 RT Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ250234; QAC80784.1;
 DR DR; AJ486836; CAD31078.1;
 DR GO; GO:0046821; C:extrachromosomal DNA; IBA.
 KW Plasmid.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;
 Query Match 32.8%; Score 20; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 PLTSV 9
 Db 2 PITQY 6
 RESULT 5
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Moloney murine sarcoma virus (Strain HT1) env/mos 5' junction
 (Fragment).
 DS Moloney murine leukemia virus.
 OC Viruses; Retroviridae; Gammaretrovirus.
 OC NCBI_TaxID=11801;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=83164305; PubMed=6300424;
 RA Donoghue D.J., Hunter T.;
 RT "Recombination junctions of variants of Moloney murine sarcomavirus:
 Generation and divergence of a mammalian transforming gene.";
 RT J. Virol. 45:607-617(1983).
 DR EMBL; K03108; AAA46494.1;
 DR NON_TER 10
 SQ SEQUENCE 10 AA; 1081 MW; 7BEFCFCBEA771B5A4 CRC64;
 Query Match 32.8%; Score 20; DB 15; Length 10;
 Best Local Similarity 75.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 8 SVPC 11
 Db 4 STPC 7
 RESULT 6
 Q56140

Q56140; PRELIMINARY;	PRT;	8 AA.		
AC Q56140; 01-NOV-1996 (TREMBLrel. 01, Created)				
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE STP6 Protein (Fragment).				
GN OS Streptococcus thermophilus.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus.				
OX NCBI_TaxID=1308;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN-ST11;				
RX MEDLINE=95047254; PubMed=7958782;				
RA Constable A.; Mollet B.;				
RT "Isolation and characterization of promoter regions from Streptococcus thermophilus."				
RT thermophilus.;				
RL FEMS Microbiol. Lett. 122:85-90(1994).				
DR EMBL; X782110; CAA55045.1; -.				
FT NON_TER 8				
SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;				
Query Match 31.1%; Score 19; DB 2; Length 8;				
Best Local Similarity 100.0%; Pred. No. 1e+06;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy 2 ISVP 5				
Db 3 ISVP 6				
RESULT 7				
Q9TKF7 PRELIMINARY;	PRT;	10 AA.		
AC Q9TKF7; 01-MAY-2000 (TREMBLrel. 13, Created)				
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE AtpB (Fragment).				
GN AtpB.				
OS Agonis grandiflora.				
OG Chloroplast.				
OC Eukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophytta; Spermatophytta; Magnoliophytta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Agonis.				
OX NCBI_TaxID=105028;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA O'Brien M.M., Quinn C.J., Wilson P.G.; "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)." ;				
RT Aust. J. Bot. 48:0-0(2000).				
RL DR EMBL; AF184675; AAC03845.1; -.				
DR GO; GO:0009507; C:chloroplast; IEA.				
KW Chloroplast.				
FT NON_TER 10				
SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;				
Query Match 31.1%; Score 19; DB 8; Length 10;				
Best Local Similarity 66.7%; Pred. No. 7.6e+03;				
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy 5 PLTSVP 10				
Db 5 PTTSRP 10				
RESULT 8				
O9TKF9 PRELIMINARY;	PRT;	10 AA.		
ID O9TKF9; 01-MAY-2000 (TREMBLrel. 13, Created)				
AC O9TKF9; 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT 01-MAY-2003 (TREMBLrel. 24, Last annotation update)				
DE AtpB (Fragment).				
GN				

OS Homalospermum firmum.
 OC Chloroplast.
 OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Homalospermum.
 RN [1]
 SEQUENCE FROM N.A.
 RP O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)." ;
 DR EMBL; AF184678; AAF03848.1; -;
 DR GO; GO:0009507; C:chloroplast ; IEA.
 RL Aust. J. Bot. 48:0-0(2000).
 FT NON TER
 SQ 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
 KW Chloroplast.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 5 PLTSVP 10
 Db 5 PTTSRP 10

RESULT 13
 Q9TKF3 PRELIMINARY; PRT; 10 AA.
 ID Q9TKF3 PRELIMINARY; PRT; 10 AA.
 AC Q9TKF3; PRELIMINARY; PRT; 10 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE AtPB (Fragment).
 GN Asteromyrtus brassii.
 OS Asteromyrtus brassii.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Asteromyrtus.
 RN [1]
 SEQUENCE FROM N.A.
 RP O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)." ;
 DR Submitted (SRP-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RA Heslewood M., Quinn C.J.;
 RA Submitted (PB-2002) to the EMBL/GenBank/DBJ databases.
 RL Submitted (PB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF184679; AAF03849.2; -;
 DR GO; GO:0009507; C:chloroplast ; IEA.
 RL Aust. J. Bot. 48:621-628 (2000).
 FT NON TER
 SQ SEQUENCE 10 AA; 1126 MW; 15132CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 5 PLTSVP 10
 Db 5 PTTSRP 10

RESULT 12
 Q9TKF4 PRELIMINARY; PRT; 10 AA.
 ID Q9TKF4 PRELIMINARY; PRT; 10 AA.
 AC Q9TKF4; PRELIMINARY; PRT; 10 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE AtPB (Fragment).
 GN Chloroplast.
 OS Angassomyrtus salina.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta;

DE AtpB (Fragment).
 GN ATPB.
 OS *Neofabricia sericisepala*.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Neofabricia.
 OX NCBI_TaxID=106055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)." ;
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184700; AAFO3869.1;
 DR GO:GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10 10 MW; 1DB12CA1B1B76440 CRC64;
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 5 PLTSVP 10
 Db 5 PTTSRP 10
 RESULT 15
 O9TKF0 PRELIMINARY; PRT; 10 AA.
 ID O9TKF0
 AC O9TKF0;
 DT 01-MAY-2000 (TREMBUREL. 13, Created)
 DT 01-MAY-2000 (TREMBUREL. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBUREL. 24, Last annotation update)
 DE AtpB (Fragment).
 GN ATPB.
 OS *Kunzea ambigua* (Tick bush).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Kunzea.
 OX NCBI_TaxID=106041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)." ;
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184683; AAFO3853.1;
 DR GO:GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10 10 MW; 1DB12CA1B1B76440 CRC64;
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 5 PLTSVP 10
 Db 5 PTTSRP 10

Search completed: September 5, 2004, 10:47:58
 Job time : 60 secs

This Page Blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:40:24 ; Search time 64 Seconds

(without alignments) 48.563 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 348779

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:
 1: GeneseqP1980s:
 2: GeneseqP1990s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003as:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	61	100.0	11	AAR04526	Aau04526 VEGF base
2	59	96.7	11	AAU04542	Aau054 VEGF base
3	57	93.4	11	AAU04545	Aau0545 VEGF base
4	54	88.5	11	AAU04543	Aau0543 VEGF base
5	52	85.2	11	AAU04544	Aau0544 VEGF base
6	45.5	74.6	10	AAU04532	Aau0532 VEGF base
7	41	67.2	9	AAU04533	Aau0533 VEGF base
8	32	52.5	9	AAU04529	Aau0529 VEGF base
9	30	49.2	8	AAR58418	Aar58418 Partial P
10	30	49.2	9	AEE34703	Aee34703 CA125/MUC
11	30	49.2	10	AAW12561	Aaw12561 SH2 bindi
12	30	49.2	11	AAW12615	Aaw12615 SH2 bindi
13	29	41.5	11	ABP47579	Abp47579 N. mening
14	29	47.5	11	ABP47580	Abp47580 N. mening
15	27	44.3	10	AAR77368	Aar77368 SH3 bindi
16	27	44.3	11	ABP47556	Abp47556 N. mening
17	26	42.6	6	AYA41619	Aya41619 Mammal
18	26	42.6	8	ARR58417	Aar58417 Partial P
19	26	42.6	9	AYB26265	Ayb26265 Isolated
20	26	42.6	9	ABR56927	Abp56927 Mouse pla
21	26	42.6	10	AAG73418	Aag73418 Human gen
22	26	42.6	10	ABG64264	Abg64264 Human alb
23	25.5	41.8	9	AAR96138	Aar96138 Procase
24	25.5	41.8	9	AAW82212	Aaw82212 D-NoxFES-
25	25.5	41.8	9	AAW46562	Aaw46562 Peptide b

26 41.0 2 AAY26264 Isolated
 27 41.0 2 AAE01112 Human leu
 28 41.0 6 AB224203 Human can
 29 41.0 6 AAE29971 Human air
 30 41.0 10 AAW01720 Inhibitor
 31 41.0 10 AAR90487 Anti
 32 41.0 10 AAW88078 Inhibitor
 33 41.0 10 AAY55214 Anti CD34
 34 41.0 10 AAU786960 Human hae
 35 41.0 10 AAU77429 Fibronect
 36 41.0 4 Aa95853 Human com
 37 41.0 10 ABR24101 Human can
 38 41.0 10 ABR24325 Human can
 39 41.0 10 ABR24347 Human can
 40 41.0 11 AAU00642 Human mem
 41 41.0 11 ADB88785 Membrane
 42 39.3 6 AAR03869 Hypotensi
 43 39.3 6 AAE05003 Human rel
 44 39.3 6 AAB60620 Human MuM
 45 39.3 7 AAU04530 VEGF base

ALIGNMENTS

RESULT 1
 AAU04526 ID AAU04526 standard; peptide; 11 AA.

XX AC AAU04526;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 3 .

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;

KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX PH Key Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

XX FT ET /note= "This bond cyclises the peptide"

XX XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis. The sequence represents a monomeric monocyclic peptide of the invention, characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, porriasis, arthropathy, hemangiomatous, vascularised malignant or benign tumour, post-angioplasty restenosis, head, heat or cold cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 11 AA;

Query Match Score 61; DB 4; Length 11;
Best Local Similarity 100.0%; Prid. No. 0.0016; AA.

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
DB 1 CISVPLTSVPC 11

RESULT 2
ID AAU04542 standard; peptide; 11 AA.
XX
AC AAU04542;
DT 26-SEP-2001 (first entry)
DE VEGF based monocyclic peptide 20.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
OS Synthetic.
FH Key Location/Qualifiers
FT Disulfide-bond 1..11 /note= "This bond cyclises the peptide"
XX PN WO200152875-A1.
PD 26-JUL-2001.
XX PF 18-JAN-2001; 2001WO-US001533.
FT /note= "This bond cyclises the peptide"
XX PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX DR WPI; 2001-442248/47.

(LUDWIG INST CANCER RES.
XX PI Achen MG, Hughes RA, Stackler S, Cendron A;
XX DR WPI; 2001-442248/47.
XX PR Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.
XX Example 25; Page 47; 102pp; English.
PS
XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residue. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, psoriasis, arthropathy, hemangiomatous, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 11 AA;

Query Match Score 59; DB 4; Length 11;
Best Local Similarity 90.9%; Prdd. No. 0.0034;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 CISVPLTSVPC 11
DB 1 CISVPLTSVPC 11

RESULT 3
ID AAU04545 standard; peptide; 11 AA.
XX
AC AAU04545;
DT 26-SEP-2001 (first entry)
DE VEGF based monocyclic peptide 23.
XX
Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
FH Key Location/Qualifiers
FT Disulfide-bond 1..11 /note= "This bond cyclises the peptide"
XX PN WO200152875-A1.
XX PD 26-JUL-2001.
XX PR 18-JAN-2001; 2001WO-US001533.
FT /note= "This bond cyclises the peptide"
XX PN WO200152875-A1.
XX PD 26-JUL-2001.
XX PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX DR WPI; 2001-442248/47.
XX PR Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

PA	(LUDW-) LUDWIG INST CANCER RES.	PN	WO200152875-A1.
XX	Achen MG, Hughes RA, Stacker S, Cendron A;	XX	
PI		PD	26-JUL-2001.
XX		XX	18-JAN-2001; 2001WO-US001533.
DR		PF	
XX		XX	18-JAN-2000; 2000US-0176293P.
PT	Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.	PR	16-MAY-2000; 2000US-0204590P.
PT		XX	(LUDW-) LUDWIG INST CANCER RES.
PT		PA	
PT		XX	
PT		XX	
PS	Example 25; Page 47; 102pp; English.	PI	Achen MG, Hughes RA, Stacker S, Cendron A;
XX		XX	
CC	The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.	PS	Page 47; 102pp; English.
CC	The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.	XX	Example 25; Page 47; 102pp; English.
CC	Sequence 11 AA;	SQ	Sequence 11 AA;
CC	Query Match 93.4%; Score 57; DB 4; Length 11; Best Local Similarity 81.8%; Pred. No. 0.0072;	CC	Query Match 88.5%; Score 54; DB 4; Length 11; Best Local Similarity 72.7%; Pred. No. 0.023;
CC	Matches 9; Conservative 2; Nismatches 0; Indels 0; Gaps 0;	CC	Matches 8; Conservative 3; Nismatches 0; Indels 0; Gaps 0;
CC		CC	
CC	QY 1 CISVPLTSVPC 11 1 : : : Db 1 CVSYPLTIVPC 11	CC	QY 1 CISVPLTSVPC 11 1 : : : : Db 1 CIRIPLTSVPC 11
CC		CC	
CC	Sequence 11 AA;	SQ	Sequence 11 AA;
CC	RESULT 4 AAU04543 ID AAU04543 standard; peptide; 11 AA.	CC	RESULT 5 AAU04544 ID AAU04544 standard; peptide; 11 AA.
CC		CC	
AC	AAU04543;	CC	
XX		XX	
DT	26-SEP-2001 (first entry)	AC	AAU04544;
XX		XX	
DB	VEGF based monocyclic peptide 21.	DT	26-SEP-2001 (first entry)
XX		XX	
KW	Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; psoriasis; tumour;	DE	VEGF based monocyclic Peptide 22.
KW	diabetes induced neovascular sequelae; rheumatoid arthritis;	XX	
KW	diabetic retinopathy; chronic inflammation; cyclic.	AC	
XX		XX	
OS	Synthetic.	XX	
XX		XX	
FH	Key Location/Qualifiers	DE	
FT	Disulfide-bond 1..11	XX	
FT	/note= "This bond cyclises the peptide"	KW	Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX		KW	

KW	diabetes induced neovascular sequelae; rheumatoid arthritis;	XX	AAU04532;
XX	diabetic retinopathy; chronic inflammation; cyclic.	XX	AC 26-SEP-2001 (first entry)
OS	Synthetic.	XX	DT 26-SEP-2001
XX		DE	VEGF based monocyclic peptide 10.
Key	Location/Qualifiers	XX	
FT Disulfide-bond	1..11 /note= "This bond cyclises the peptide"	XX	Human; VEGF; vascular endothelial growth factor; angiogenesis;
FT		XX	KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
PN	WO200152875-A1.	XX	KW diabetes induced neovascular sequelae; rheumatoid arthritis;
XX		XX	KW diabetic retinopathy; chronic inflammation; cyclic.
PD	26-JUL-2001.	OS	
XX		XX	Synthetic.
PP	18-JAN-2001; 2001WO-US001513.	XX	Key Location/Qualifiers
XX	PR 18-JAN-2000; 2000US-0176293P.	XX	FT 1..10
PR	16-MAY-2000; 2000US-0204590P.	FT	/note= "This bond cyclises the peptide"
XX		XX	
PA	(LUDW-) LUDWIG INST CANCER RES.	XX	
XX		XX	
PI	Achen MG, Hughes RA, Stacke S, Cendron A;	XX	
XX	PD 26-JUL-2001.	XX	
WPI:	2001-442248/47.	XX	
XX		XX	18-JAN-2001; 2001WO-US001533.
PR	Novel monomeric monocyclic peptide, used to interfere with angiogenesis,	XX	PR 18-JAN-2000; 2000US-0176293P.
PR	or lymphangiogenesis, is produced by cyclizing a peptide loop fragment	XX	PR 16-MAY-2000; 2000US-0204590P.
PR	from an exposed loop of a growth factor protein by oxidizing the cysteine	XX	(LUDW-) LUDWIG INST CANCER RES.
PR	residues.	XX	
XX	Example 25; Page 47; 102pp; English.	XX	
PS	The sequence represents a monomeric monocyclic peptide of the invention,	XX	Claim 49; Page 32; 102pp; English.
CC	whose 3 dimensional structure is modelled on the expose loop of human	XX	The sequence represents a monomeric monocyclic peptide of the invention,
CC	VEGFD (vascular endothelial growth factor). The invention relates to a	CC	whose 3-dimensional structure is modelled on the expose loop of human
CC	method of producing a monomeric monocyclic peptide by a measuring beta-	CC	VEGFD (vascular endothelial growth factor) . The invention relates to a
CC	beta carbon separation on opposite antiparallel strands of a	CC	method of producing a monomeric monocyclic peptide by a measuring beta-
CC	peptide loop fragment from an exposed loop of a growth factor protein and	CC	beta carbon separation on opposite antiparallel strands of a
CC	cyclising the peptide by oxidising the cysteine residues. The monomeric	CC	peptide loop fragment from an exposed loop of a growth factor protein and
CC	peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic	CC	cyclising the peptide by oxidising the cysteine residues. The monomeric
CC	peptides), and a cyclic peptide with at least one amino acid deleted prior	CC	peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC	to cyclising are used to interfere with angiogenesis,	CC	peptides), and a cyclic peptide with at least one amino acid deleted prior
CC	neovascularisation or lymphangiogenesis in a mammal with a condition	CC	to cyclising are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis.
CC	characterised by angiogenesis, neovascularisation or lymphangiogenesis.	CC	The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-
CC	The condition is diabetic retinopathy, psoriasis, arthropathy,	CC	beta carbon separation on opposite antiparallel strands of a
CC	hemangoma, vascular accident, post-angioplasty restenosis, head, heat or cold	CC	peptide loop fragment from an exposed loop of a growth factor protein and
CC	cerebrovascular accident, post-angioplasty restenosis, head, heat or cold	CC	cyclising the peptide by oxidising the cysteine residues. The monomeric
CC	trauma, substance-induced neovascularisation of the liver, excessive	CC	peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC	hormone-related angiogenic dysfunction, diabetes induced neovascular	CC	peptides) and a cyclic peptide with at least one amino acid deleted prior
CC	sequela, hypertension induced neovascular sequelae, or chronic liver	CC	to cyclising are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition
CC	infection. The peptides are also used to modulate vascular permeability	CC	characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC	in a mammal (the mammal has a condition characterised by fluid	CC	The condition is diabetic retinopathy, psoriasis, arthropathy,
CC	accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,	CC	hemangoma, vascular malignant or benign tumour, post-recovery
CC	or brain. The peptides are used to image blood vessels and lymphatic	CC	cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC	vasculature. The monomeric and bicyclic peptides are used to interfere	CC	trauma, substance-induced neovascularisation of the liver, excessive
CC	with at least one biological activity induced by VEGF, VEGF-C or -D and	CC	hormone-related angiogenic dysfunction, diabetes induced neovascular
CC	chronic inflammation, especially rheumatoid arthritis, psoriasis and	CC	sequela, hypertension induced neovascular sequelae, or chronic liver
CC	diabetic retinopathy	CC	infection. The peptides are also used to modulate vascular permeability
XX	Sequence 11 AA;	CC	in a mammal (the mammal has a condition characterised by fluid
SQ	Query Match 1 CISVPLTSVPC 11	CC	accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
Best Local Similarity 0.99;	Score 52; DB 4; Length 11;	CC	or brain. The peptides are used to image blood vessels and lymphatic
Matches 10;	Pred. No. 0.049;	CC	vasculature. The monomeric and bicyclic peptides are used to interfere
Conservative 3;	Mismatches 0;	CC	with at least one biological activity induced by VEGF, VEGF-C or -D and
Db	Indels 0;	CC	chronic inflammation, especially rheumatoid arthritis, psoriasis and
	Gaps 0;	CC	diabetic retinopathy
QY	1 CISVPLTSVPC 11	XX	Sequence 10 AA;
	: :	SQ	Query Match 1 CISLPISSVPC 11
			Best Local Similarity 0.99;
			Score 45.5; DB 4; Length 10;
			Pred. No. 0.52;
			Mismatches 0;
			Indels 1;
			Gaps 1;
RESULT 6			
AAU04532			
ID AAU04532	standard; peptide; 10 AA.		

CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX SQ Sequence 9 AA;

RESULT 7
 AAU04533 standard; peptide: 9 AA.
 ID AAU04533
 AC AAU04533;
 XX DT 26-SEP-2001 (first entry)
 DB VEGF based monocyclic peptide 11.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Disulfide-bond 1..9
 FT /note= "This bond cyclises the peptide"
 XX PN WO200152875-A1.
 XX PD 26-JUL-2001.
 XX PP 18-JAN-2001; 2001WO-US001533.
 PR 18-JAN-2000; 2000US-0176793P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDWIG) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stackler S, Cendron A;
 XX DR WPI; 2001-442248/47.
 XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX PS Claim 49; Page 32; 102pp; English.
 XX CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and

Query Match 67.2%; Score 41; DB 4; Length 9;
 Best Local Similarity 81.8%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Index 2; Gaps 1;
 SQ Sequence 9 AA;

RESULT 8
 AAU04529 standard; peptide: 9 AA.
 ID AAU04529
 XX AC AAU04529;
 XX DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 7.
 DE XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Disulfide-bond 1..9
 FT /note= "This bond cyclises the peptide"
 XX PN WO200152875-A1.
 XX PD 26-JUL-2001.
 XX PR 18-JAN-2001; 2001WO-US001533.
 PR 16-MAY-2000; 2000US-0176793P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDWIG) LUDWIG INST CANCER RES.
 XX PS Claim 49; Page 32; 102pp; English.

Claim 49; Page 32; 102pp; English.
 XX CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and

CC trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs, Fcritoneal or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGP-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 9 AA;

SQ Query Match 52.5%; Score 32; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9

Db 2 SVPLTSV 8

RESULT 9
ID AAR58418 Standard; protein: 8 AA.

XX AAR58418;

XX DT 25-MAR-2003 (revised)

DT 13-APR-1995 (first entry)

XX Partial Peptide 7 from TSAR C46.9-2 binding domain.

XX TSAR: totally synthetic affinity reagent; synthetic; binding domain;

XX effector domain; concatenated heterofunctional protein; linker; direct;

XX rapid; detection; screening; treatment; monoclonal antibody; Mab; C46;

XX anti-carcinoembryonic antigen; anti-CEA.

XX OS Synthetic.

XX PN WO9418318-A1.

XX PD 18-AUG-1994.

XX PF 01-FEB-1994; 94WO-US000977.

XX PR 01-FEB-1993; 93US-00013416.

PR 30-DEC-1993; 93US-00176500.

PR 31-JAN-1994; 94US-00189331.

XX PA (UNNC-) UNIV NORTH CAROLINA.

PA Kay BK, Fowlkes DM;

XX DR; 1994-279739/34.

XX Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain.

XX Example 7.5; Page 108; 255pp; English.

XX PS DR; 1994-279739/34.

XX Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain.

XX Example 7.5; Page 108; 255pp; English.

XX CC ARS8412-42 are overlapping 8-mer peptides of the binding domain of TSAR

CC (Totally Synthetic Affinity Reagents) peptide TSAR C46.9-2 (ARS8411).

CC These bind (partially) a monoclonal antibody, i.e. anti-CEA C46 (anti-CC carcinoembryonic antigen). TSAR peptides are generated using generic CC oligonucleotides (see AAQ7 0470-73 for examples). TSARs are concatenated CC heterofunctional proteins or peptides, comprising at least two functional CC regions - a binding domain with affinity for a ligand and a second CC effector peptide portion that is chemically or biologically active. They CC may further comprise a linker peptide between the 2 domains. The TSARs or

CC compns. comprising a TSAR binding domain can be used in vivo to deliver
CC a chemically or biologically active moiety, e.g. metal ion, radioisotope,
CC peptide, toxin or enzyme, to the specific target or on the cell. They can
CC also replace the function of macromolecules eg. monoclonal or polyclonal
CC antibodies and therefore circumvent the need for complex methods of
CC hybridoma formation or in vivo antibody production. The TSARs are easily
CC characterised and have designed activity allowing direct and rapid
CC detection in a screening process. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;

Best Local Similarity 62.5%; Prod. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OS Neisseria meningitidis.
OS Synthetic.

XX WO200228888-A2.
XX PD 11-APR-2002.
XX PP 03-OCT-2001; 2001WO-EP011409.
XX PR 03-OCT-2000; 2000GB-00024200.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI De Boille XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;
DR 2002-479596/51.
PR Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody.

XX Claim 15; Page 43; 55pp; English.

CC The present invention describes mimotopes (I) of a surface L3, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis comprising a peptide epitope obtained by screening a peptide library with a monoclonal antibody (Mab) like 4BE12C10, H44/24, H44/58, H44/70 or H44/78. (I) is antigenically cross-reactive with Mab. (I) have antibacterial and antiinflammatory activities, and can be used in vaccines. Mab is useful in the identification of (I). (I) or Mab are useful as a medicament, and also in the manufacture of a medicament for treating or preventing meningococcal disease. (I) and Mab are useful for treating a patient suffering from or susceptible to meningococcal disease by administering (I) or Mab to the patient. (I) is useful in a diagnostic assay for meningococcal infection to detect antibodies against L3, 7, 9, LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754 represent sequences used in the exemplification of the present invention

PS Sequence 11 AA;

XX Query Match Score 29; DB 5; Length 11;
CC Best Local Similarity 27.3%; Pred. No. 3.1e+02;
CC Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
CC ID AAR7368 standard; peptide; 10 AA.
XX AC AAR7368;
XX DT 17-JAN-1996 (first entry)
XX DE SH3 binding domain CAIR-1 B.
XX KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;
XX Src homology 3; SH3 binding domain.
XX OS Homo sapiens.
XX PN WO9525125-A1.
XX PD 21-SEP-1995.
XX PF 14-MAR-1995; 95WO-US003610.
XX PR 14-MAR-1994; 94US-00212190.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kohn EC, Liotta LA, Kim YS;
XX DR WPI; 1995-336944/43.
XX PT DNA encoding CAI resistance proteins - used in gene therapy, and for detecting CAI resistance in biological samples.

XX DNA encoding CAI resistance proteins - used in gene therapy, and for detecting CAI resistance in biological samples.

XX WO200228888-A2.
XX PD 11-APR-2002.
XX PR 03-OCT-2001; 2001WO-EP011409.

PR 03-OCT-2000; 2000GB-00024200.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI De Boille XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;
XX DR 2002-479596/51.
PR Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody.

XX Claim 15; Page 43; 55pp; English.

CC The present invention describes mimotopes (I) of a surface L3, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis comprising a peptide epitope obtained by screening a peptide library with a monoclonal antibody (Mab) like 4BE12C10, H44/24, H44/58, H44/70 or H44/78. (I) is antigenically cross-reactive with Mab. (I) have antibacterial and antiinflammatory activities, and can be used in vaccines. Mab is useful in the identification of (I). (I) or Mab are useful as a medicament, and also in the manufacture of a medicament for treating or preventing meningococcal disease. (I) and Mab are useful for treating a patient suffering from or susceptible to meningococcal disease by administering (I) or Mab to the patient. (I) is useful in a diagnostic assay for meningococcal infection to detect antibodies against L3, 7, 9, LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754 represent sequences used in the exemplification of the present invention

PS Sequence 11 AA;

XX Query Match Score 29; DB 5; Length 11;
CC Best Local Similarity 36.4%; Pred. No. 3.1e+02;
CC Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
CC ID AAR7368 standard; peptide; 10 AA.
XX AC AAR7368;
XX DT 17-JAN-1996 (first entry)
XX DE SH3 binding domain CAIR-1 B.
XX KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;
XX Src homology 3; SH3 binding domain.
XX OS Homo sapiens.
XX PN WO9525125-A1.
XX PD 21-SEP-1995.
XX PF 14-MAR-1995; 95WO-US003610.
XX PR 14-MAR-1994; 94US-00212190.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kohn EC, Liotta LA, Kim YS;
XX DR WPI; 1995-336944/43.
XX PT DNA encoding CAI resistance proteins - used in gene therapy, and for detecting CAI resistance in biological samples.

XX DNA encoding CAI resistance proteins - used in gene therapy, and for detecting CAI resistance in biological samples.

XX WO200228888-A2.
XX PD 11-APR-2002.
XX PR 03-OCT-2001; 2001WO-EP011409.

PS Example 4; Page 40; 56pp; English.
XX CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human
CC melanoma cells, contains a unique proline-rich sequence which fulfills
CC the consensus definition for Src homology 3 (SH3) binding proteins
CC (AAR77366). 4 Unique versions (AAR77367-70) are present
XX Sequence 10 AA;

Query Match 44.3%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 6e-02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 VPIITSVPC 11
Db 1 VPPAPVPC 8

Search completed: September 5, 2004, 10:46:32
Job time : 66 secs

This page blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.
GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:46:55 ; Search time 67 Seconds

51.727 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters:

171292

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:^{*}

1: /cgn2_6_ptodata/2/pubpa/us07_pubcomb.pep:
 2: /cgn2_6_ptodata/2/pubpa/us07_pubcomb.pep:
 3: /cgn2_6_ptodata/2/pubpa/us06_pubcomb.pep:
 4: /cgn2_6_ptodata/2/pubpa/us06_pubcomb.pep:
 5: /cgn2_6_ptodata/2/pubpa/us07_pubcomb.pep:
 6: /cgn2_6_ptodata/2/pubpa/us07_pubcomb.pep:
 7: /cgn2_6_ptodata/2/pubpa/us08_pubcomb.pep:
 8: /cgn2_6_ptodata/2/pubpa/us08_pubcomb.pep:
 9: /cgn2_6_ptodata/2/pubpa/us09_pubcomb.pep:
 10: /cgn2_6_ptodata/2/pubpa/us09_pubcomb.pep:
 11: /cgn2_6_ptodata/2/pubpa/us09_pubcomb.pep:
 12: /cgn2_6_ptodata/2/pubpa/us09_pubcomb.pep:
 13: /cgn2_6_ptodata/2/pubpa/us10_pubcomb.pep:
 14: /cgn2_6_ptodata/2/pubpa/us10_pubcomb.pep:
 15: /cgn2_6_ptodata/2/pubpa/us10_pubcomb.pep:
 16: /cgn2_6_ptodata/2/pubpa/us10_pubcomb.pep:
 17: /cgn2_6_ptodata/2/pubpa/us10_pubcomb.pep:
 18: /cgn2_6_ptodata/2/pubpa/us10_pubcomb.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	61	100.0	11 9 US-09-761-636A-7	Sequence 7, Appli
2	59	96.7	11 9 US-09-761-636A-23	Sequence 23, Appli
3	57	93.4	11 9 US-09-761-636A-26	Sequence 26, Appli
4	54	88.5	11 9 US-09-761-636A-24	Sequence 24, Appli
5	52	85.2	11 9 US-09-761-636A-25	Sequence 25, Appli
6	45.5	74.6	10 9 US-09-761-636A-13	Sequence 13, Appli
7	41	67.2	9 9 US-09-761-636A-14	Sequence 14, Appli
8	32	52.5	9 9 US-09-761-636A-10	Sequence 10, Appli
9	29	47.5	9 12 US-10-253-286-332	Sequence 332, Appli
10	29	47.5	9 15 US-10-245-871-332	Sequence 332, Appli
11	29	47.5	11 12 US-10-398-104-155	Sequence 155, Appli
12	29	47.5	11 12 US-10-398-104-156	Sequence 156, Appli
13	29	47.5	11 14 US-10-126-845-89	Sequence 89, Appli
14	28	45.9	9 15 US-10-154-884B-11221	Sequence 11221, A
15	27	44.3	9 15 US-10-154-884B-11228	Sequence 11228, A

Length	Query ID	Match ID	Description
11	US-09-761-636A-7	US-09-761-636A-7	Sequence 7, Appli
11	US-09-761-636A-23	US-09-761-636A-23	Sequence 23, Appli
11	US-09-761-636A-26	US-09-761-636A-26	Sequence 26, Appli
11	US-09-761-636A-24	US-09-761-636A-24	Sequence 24, Appli
11	US-09-761-636A-25	US-09-761-636A-25	Sequence 25, Appli
10	US-09-761-636A-13	US-09-761-636A-13	Sequence 13, Appli
9	US-09-761-636A-14	US-09-761-636A-14	Sequence 14, Appli
9	US-09-761-636A-10	US-09-761-636A-10	Sequence 10, Appli
9	US-10-253-286-332	US-10-253-286-332	Sequence 332, Appli
9	US-10-245-871-332	US-10-245-871-332	Sequence 332, Appli
11	US-10-398-104-155	US-10-398-104-155	Sequence 155, Appli
11	US-10-398-104-156	US-10-398-104-156	Sequence 156, Appli
11	US-10-126-845-89	US-10-126-845-89	Sequence 89, Appli
15	US-10-154-884B-11221	US-10-154-884B-11221	Sequence 11221, A
15	US-10-154-884B-11228	US-10-154-884B-11228	Sequence 11228, A

RESULT 1
US-09-761-636A-7
; Application US/09761636A
; Patent No. US2002006518A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF-C PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505
; CURRENT FILING DATE: 2001-01-18
; PRIORITY NUMBER: US 60/176,293
; PRIORITY NUMBER: US 60/176,293
; PRIORITY NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

RESULT 2
US-09-761-636A-23
; Application US/09761636A
; Patent No. US2002006518A1
; CURRENT FILING DATE: 2000-05-16
; PRIORITY NUMBER: US 60/176,293
; PRIORITY NUMBER: US 60/176,293
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

ALIGNMENTS

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 11; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
Db 1 CISVPLTSVPC 11

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-08
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 23
LENGTH: 11
TYPE: PRT
ORGANISM: synthetic construct
us-09-761-636A-23

Query Match Score 96.7%; Pred. No. 0.0074; Length 11;
Best Local Similarity 90.9%; Mismatches 0; Indels 0;
Matches 10; Conservative 1; Gaps 0;

Qy 1 CISYPLTSVPC 11
Db 1 CLSYPLTSVPC 11

RESULT 3
US-09-761-636A-26

; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 26
LENGTH: 11
TYPE: PRT
ORGANISM: synthetic construct
us-09-761-636A-26

Query Match Score 93.4%; Pred. No. 0.015; Length 11;
Best Local Similarity 81.8%; Mismatches 0; Indels 0;
Matches 9; Conservative 2; Gaps 0;

Qy 1 CISYPLTSVPC 11
Db 1 CVSPLTSTVPC 11

RESULT 4
US-09-761-636A-24

; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293

GENERAL INFORMATION:
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
; US-09-761-636A-24

Query Match Score 88.5%; Pred. No. 0.046; Length 11;
Best Local Similarity 72.7%; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 3; Gaps 0;

Qy 1 CISYPLTSVPC 11
Db 1 CITPLTSLPC 11

RESULT 5
US-09-761-636A-25

; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 25
LENGTH: 11
TYPE: PRT
ORGANISM: synthetic construct
US-09-761-636A-25

Query Match Score 85.2%; Pred. No. 0.095; Length 11;
Best Local Similarity 72.7%; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISYPLTSVPC 11
Db 1 CISPLTSVPC 11

RESULT 6
US-09-761-636A-13

; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293

```

; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 6 0/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 74.6%; Score 45.5; DB 9; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CISVPLNSVPC 11
Db 1 CISVPL-SVPC 10

RESULT 7
US-09-761-636A-14
Sequence 14, Application US/09761636A
Patent No. US20065218A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 14
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match 67.2%; Score 41; DB 9; Length 9;
Best Local Similarity 81.8%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Qy 1 CISVPLNSVPC 11
Db 1 CISVPL-SVPC 9

RESULT 8
US-09-761-636A-10
Sequence 10, Application US/09761636A
Patent No. US2006518A1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0

Query Match 52.5%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SVPLTSV 9
Db 2 SVPLTSV 8

RESULT 9
US-10-253-286-332
Sequence 332, Application US/10253286
Publication No. US004005881A1
GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
TITLE OF INVENTION: Ti-KERY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: FEH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 332
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-253-286-332

Query Match 47.5%; Score 29; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 VPLTSVP 10
Db 2 VPITSVP 8

RESULT 10
US-10-245-871-332
Sequence 332, Application US/10245871
Publication No. US2003023594A1
GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
TITLE OF INVENTION: Ti-KERY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 332
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-245-871-332

Query Match 47.5%; Score 29; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

Qy 4 VPLTSVP 10
Db 2 VPITSTP 8

RESULT 11
US-10-398-104-155
Sequence 155, Application US/10398104
Publication No. US20040047880A1
GENERAL INFORMATION:
APPLICANT: De Bolle, Xavier Thomas
APPLICANT: Letesson, Jean-Jacques
APPLICANT: Lobet, Yves
APPLICANT: Mertens, Pascal Yvon
APPLICANT: Poolman, Jan
APPLICANT: Voet, Pierre
TITLE OF INVENTION: COMPONENT FOR VACCINE
FILE REFERENCE: B4242
CURRENT APPLICATION NUMBER: US/10/398,104
CURRENT FILING DATE: 2003-01-04
PRIOR APPLICATION NUMBER: PCT/EP01/11409
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: GB 0024200.8
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 352
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 155
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-155

Query Match 47.5%; Score 29; DB 12; Length 11;
Best Local Similarity 27.3%; Pred. No. 4.2e+02;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
Db 1 CTVTPYRGQG 11

RESULT 12
US-10-398-104-156
Sequence 156, Application US/10398104
Publication No. US20040047880A1
GENERAL INFORMATION:
APPLICANT: De Bolle, Xavier Thomas
APPLICANT: Letesson, Jean-Jacques
APPLICANT: Lobet, Yves
APPLICANT: Mertens, Pascal Yvon
APPLICANT: Poolman, Jan
APPLICANT: Voet, Pierre
TITLE OF INVENTION: COMPONENT FOR VACCINE
FILE REFERENCE: B45242
CURRENT APPLICATION NUMBER: US/10/398,104
CURRENT FILING DATE: 2003-01-04
PRIOR APPLICATION NUMBER: PCT/EP01/11409
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: GB 0024200.8
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 352
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 156
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-156

Query Match 47.5%; Score 29; DB 12; Length 11;
Best Local Similarity 36.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
Db 1 CFAPPXDLPLC 11

RESULT 13
US-10-126-845-89
Sequence 89, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Inelda J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Houghton, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/2005B
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO: 89
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D form Peptide
FEATURE:
NAME/KEY: MISCE_FEATURE
LOCATION: (11):(11)
OTHER INFORMATION: D form retroinversion peptide
US-10-126-845-89

Query Match 47.5%; Score 29; DB 14; Length 11;
Best Local Similarity 45.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
Db 1 CLLVPLLYAAC 11

RESULT 14
US-10-154-884B-11221
Sequence 11221, Application US/10154884B
Publication No. US2004005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane A.
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-01352IUS
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 60/185,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR FILING DATE: 2000-05-04
 PRIOR APPLICATION NUMBER: US 60/206,201
 PRIOR FILING DATE: 2000-05-22
 PRIOR APPLICATION NUMBER: US 60/218,950
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 60/222,903
 PRIOR FILING DATE: 2000-08-03
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 11290
 SEQ ID NO: 11221
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-154-884B-11221

Query Match 45.9%; Score 28; DB 15; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.2e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CISVPLT 7
 Db 2 CLSVPVS 8

RESULT 15
 US-10-154-884B-11228
 Sequence 11228, Application US/10154884B
 Publication No. US20040005561A1
 GENERAL INFORMATION:
 APPLICANT: Gaiger, Alexander
 ALGATE, Paul A.
 APPLICANT: Mannion, Jane
 APPLICANT: Retter, Marc W.
 APPLICANT: Corixa Corporation
 TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
 TITLE OF INVENTION: Hematological Malignancies
 FILE REFERENCE: 014088-013521US
 CURRENT APPLICATION NUMBER: US/10/154,884B
 CURRENT FILING DATE: 2002-05-23
 PRIOR APPLICATION NUMBER: US 60/186,126
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: US 60/190,479
 PRIOR FILING DATE: 2000-03-17
 PRIOR APPLICATION NUMBER: US 60/200,545
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: US 60/200,303
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: US 60/200,779
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: US 60/200,999
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: US 60/202,084
 PRIOR FILING DATE: 2000-05-04
 PRIOR FILING DATE: 2000-05-22
 PRIOR APPLICATION NUMBER: US 60/218,950
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 60/222,903
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 11290
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 11228
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-154-884B-11228

Query Match 41.3%; Score 27; DB 15; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Search completed: September 5, 2004, 10:52:48
 Job time : 67 secs

This Page Blank (uspto)

USPTO

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:45:30 ; Search time 20 Seconds

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625931 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgnd_6/prodata/2/iaa/5A_COMB.pep:
 2: /cgnd_6/prodata/2/iaa/5B_COMB.pep:
 3: /cgnd_6/prodata/2/iaa/6A_COMB.pep:
 4: /cgnd_6/prodata/2/iaa/6B_COMB.pep:
 5: /cgnd_6/prodata/2/iaa/PCFTUS_COMB.pep:
 6: /cgnd_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	49.2	8	1 US-09-189-331-150	Sequence 150, App
2	30	49.2	8	2 US-09-471-068-150	Sequence 150, App
3	27	44.3	10	1 US-09-212-190A-5	Sequence 5, Appli
4	27	44.3	10	2 US-09-321-5	Sequence 5, Appli
5	27	44.3	10	5 PCT-US55-0610-5	Sequence 5, Appli
6	26	42.6	6	2 US-09-769-045-15	Sequence 15, Appli
7	26	42.6	8	1 US-09-189-331-149	Sequence 149, App
8	25	41.8	8	2 US-09-471-068-149	Sequence 33, Appli
9	25.5	41.8	9	1 US-09-331-183-33	Sequence 108, App
10	25.5	41.8	9	1 US-09-549-008-43	Sequence 108, App
11	25.5	41.8	9	3 US-09-802-981-143	Sequence 143, Appli
12	25	41.0	8	1 US-09-360-139B-1	Sequence 1, Appli
13	25	41.0	10	2 US-09-483-077C-26	Sequence 26, Appli
14	25	41.0	10	2 US-09-519-109B-26	Sequence 108, App
15	25	41.0	10	3 US-09-482-528-108	Sequence 108, App
16	25	41.0	10	5 PCT-US55-10811-38	Sequence 38, Appli
17	25	41.0	10	5 PCT-US55-10811-38	Sequence 21, Appli
18	24	39.3	6	1 US-09-183-134A-21	Sequence 30, Appli
19	24	39.3	6	3 US-09-476-134A-30	Patent No. 5150920
20	24	39.3	6	6 5190920-26	Patent No. 5506208
21	24	39.3	6	6 5506208-28	Sequence 1, Appli
22	24	39.3	7	4 US-09-438-150-1	Sequence 154, App
23	24	39.3	9	2 US-09-440-183-154	Sequence 204, App
24	24	39.3	9	4 US-09-601-729-204	Sequence 187, App
25	24	39.3	10	3 US-09-836-075A-187	Sequence 31, Appli
26	23.5	38.5	9	1 US-09-331-183-31	Sequence 42, Appli
27	23.5	38.5	9	1 US-09-549-008-42	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-189-331-150
; Sequence 150, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-5090
; TELEFAX: 212 863-864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-189-331-150
Query Match 1 CISYPLTS 8
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0;
Gaps 0;

RESULT 2
 US-08-471-068-150
 Sequence 150, Application US/08471068
 Patent No. 59,88635
 GENERAL INFORMATION:
 APPLICANT: Kay, B. K.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 NUMBER OF SEQUENCES: 186
 CORRESPONDENCE ADDRESS:
 ADDRESS: Penne & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10016-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,068
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEX: 66141 PENNIE
 INVENTORY FOR SEQ ID NO: 150:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-471-068-150

Query Match 49.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 62.5%; Pred. No. 3e-05; Indels 2; Gaps 0;
 Matches 5; Conservative 1; Mismatches 10;

QY 1 CISVPLTS 8
 DB 1 CVSAPQTS 8

RESULT 3
 US-08-212-190A-5
 Sequence 5, Application US/08212190A
 Patent No. 5652233
 GENERAL INFORMATION:
 APPLICANT: KOHN, Elise C.
 APPLICANT: LIOTTA, Lance A.
 APPLICANT: KIM, Young Sook
 TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: Stewart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/212,190A
 FILING DATE: 14-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 15280-204US
 REFERENCE/DOCKET NUMBER: DHS Ref. No. 5652223 E-112-94/0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9800
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-212-190A-5

Query Match 44.3%; Score 27; DB 1; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPITSYPC 11
 Db 1 VPPAVPVC 8

RESULT 4
 US-08-900-321-5
 Sequence 5, Application US/08900321
 Patent No. 5981712
 GENERAL INFORMATION:
 APPLICANT: Kohn, Elise C.
 APPLICANT: Liotta, Lance A.
 APPLICANT: Kim, Young S.
 TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
 Title of Invention: Uses Thereof
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/900,321
 FILING DATE: 25-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-204100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-900-321-5

Query Match 44.3%; Score 27; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VPLTSVPC 11
 Db 1 VPPAPVPC 8

RESULT 5
 PCT-US95-03610-5

Sequence 5, Application PC/TUS9503610
 GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND USES THEREOF
 NUMBER OF SEQUENCES: 10
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/03610
 FILING DATE: 14-MAR-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/7212,190
 FILING DATE: 14-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 31,677
 REFERENCE/DOCKET NUMBER: 15280-2040000PC
 REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0
 TELECOMMUNICATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 PCT-US95-03610-5

SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match 44.3%; Score 27; DB 5; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VPLTSVPC 11
 Db 1 VPPAPVPC 8

RESULT 6
 US-08-769-745-15

Sequence 15, Application US/08769745
 GENERAL INFORMATION:
 APPLICANT: Holmes, Todd C.
 APPLICANT: Levitan, Irwin B.
 TITLE OF INVENTION: Mechanism for the Regulation of Ion Channel Activity
 TITLE OF INVENTION: Channel Activity

RESULT 7
 US-08-189-331-149

Sequence 149, Application US/08189331
 Patent No. 5747334
 GENERAL INFORMATION:
 APPLICANT: Kay, B. K.
 APPLICANT: Powikes, D. M.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 NUMBER OF SEQUENCES: 186
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Pennie & Edmonds
 STREET: 1115 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZLFB: 10036-2711
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/189,331
 FILING DATE: Concurrently herewith
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-155
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 859-8844/9741
 TELEX: 66141 PENNIE
 SEQUENCE FOR SEQ ID NO: 149:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

Query Match 42.6%; Score 26; DB 1; Length 8;
 Best Local Similarity 57.1%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CISVPLT 7
 Db 2 CVSAPCT 8

RESULT 8
 US-08-471-068-149

Sequence 149 Application US/08471068
 Patent No. 5948635
 GENERAL INFORMATION:
 APPLICANT: KAY, B.
 APPLICANT: Fowlkes, D. M.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagent B
 NUMBER OF SEQUENCES: 186
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penning & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,068
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/189,331
 REGISTRATION NUMBER: 18,872
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 569-8864/9741
 TELEX: 66141 BENNIE
 INFORMATION FOR SEQ ID NO: 149:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-471-068-149

Query Match Score 42.6%; Score 26; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 3e+05; 2; Indels 0; Gaps 0;

Qy 1 CISVPLT 7
 Db 2 CVSAFQT 8

US-08-331-383-33
 Sequence 33, Application US/08331383
 GENERAL INFORMATION:
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly S.
 TITLE OF INVENTION: Compositions for the Detection of
 Title of Invention: Processes in Biological Samples and Methods and Use
 Title of Invention: Thereof
 Number of Sequences: 56
 Correspondence Address:
 Addressee: Townsend and Townsend Khorrie and Crew
 Street: One Market Plaza, Steuart Tower, Suite 2000
 City: San Francisco
 State: California
 Country: USA
 Zip: 94105
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible

US-08-331-383-33
 Sequence 33, Application US/08331383
 GENERAL INFORMATION:
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly S.
 TITLE OF INVENTION: Compositions for the Detection of
 Title of Invention: Processes in Biological Samples and Methods and Use
 Title of Invention: Thereof
 Number of Sequences: 56
 Correspondence Address:
 Addressee: Townsend and Townsend Khorrie and Crew
 Street: One Market Plaza, Steuart Tower, Suite 2000
 City: San Francisco
 State: California
 Country: USA
 Zip: 94105
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331,383
 FILING DATE: 28-OCT-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 16885-1
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-331-383-33

Query Match Score 41.8%; Score 25.5; DB 1; Length 9;
 Best Local Similarity 44.4%; Pred. No. 3e+05; 0; Indels 1; Gaps 1;
 Matches 4; Conservative 4; Mismatches 0;

Qy 3 SYPLTSYPC 11
 Db 2 AIPM-SIPEC 9

RESULT 10
 US-08-549-008-43
 Sequence 43, Application US/08549008
 Patent No. 5714342
 GENERAL INFORMATION:
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly S.
 TITLE OF INVENTION: Compositions for the Detection of f
 TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 Addressee: Townsend and Townsend and Crew LLP
 Street: Two Embarcadero Center, Eighth Floor
 City: San Francisco
 State: California
 Zip: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/549,008
 FILING DATE: 27-OCT-1995
 CLASSIFICATION: 435
 PRIMER APPLICATION DATA:
 APPLICATION NUMBER: US 08/331,383
 FILING DATE: 28-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 016885-000110US
 TELECOMMUNICATION INFORMATION:
 Telephone: (415) 576-0200
 Telefax: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 US-08-549-008-43

Query Match Score 25.5; DB 1; Length 9;
 Best Local Similarity 41.8%; Pred. No. 3e+05;
 Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 3 SVPLTSVPC 11
 Db 2 AIPM-SIPC 9

RESULT 11
 US-08-981-143
 ; Sequence 143, Application US/0802981
 ; Patent No. 607137

GENERAL INFORMATION:
 ; APPLICANT: Komoriya, Akira
 ; TITLE OF INVENTION: Compositions for the Detection of Enzyme Activity in Biological Samples and Methods of Use Thereof
 ; NUMBER OF SEQUENCES: 231
 ; TITLE OF INVENTION: Activity in
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-1834

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/802,981
 ; FILING DATE: 20-FEB-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom
 ; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 016865-000300US
 ; TELECOMMUNICATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 143:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-981-143

Query Match Score 25.5; DB 3; Length 9;
 Best Local Similarity 41.8%; Pred. No. 3e+05;
 Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 3 SVPLTSVPC 11
 Db 2 AIPM-SIPC 9

RESULT 12
 US-08-360-239B-1
 ; Sequence 1, Application US/08360239B
 ; Patent No. 5801222

GENERAL INFORMATION:
 ; APPLICANT: Pettit, George R.
 ; TITLE OF INVENTION: Isolation and Structure of the Human Cancer Cell Growth Inhibitory Cyclic Octapeptides Phakellistatin 10 and 11

Query Match Score 25.5; DB 1; Length 8;
 Best Local Similarity 41.0%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PLTSPV 10
 Db 1 PLTPIP 6

RESULT 13
 US-08-483-077C-26
 ; Sequence 26, Application US/08483077C
 ; Patent No. 5811391

GENERAL INFORMATION:
 ; APPLICANT: Arrhenius, Thomas S.
 ; APPLICANT: Tempczyk, Anna
 ; APPLICANT: Elices, Mariano J.
 ; APPLICANT: Zheng, Zhong-Li
 ; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics, Compositions and Methods of Using Same
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
 STATE: California
 ZIP: 92122
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,077C
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-CV 1647
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEX/FAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 10
 OTHER INFORMATION: /note= "The carboxy-terminus is a
 carboxamide."
 US-08-483-077C-26

Query Match Score 25; DB 2; Length 10;
 Best Local Similarity 44.4%; Pred. No. 3.e+02;
 Matches 4; Conservative 3; Indels 0;
 Gaps 0;

Qy 2 ISVPLTSVP 10
 Db 2 LDVPLLDVP 10

RESULT 14
 US-08-519-109B-26
 Sequence 26, Application US/08519109B
 Patent No. 5869448
 GENERAL INFORMATION:
 APPLICANT: Arrhenius, Thomas S.
 APPLICANT: Tempczyk, Anna J.
 APPLICANT: Blices, Mariano J.
 APPLICANT: Zheng, Zhong-Li
 TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
 TITLE OF INVENTION: Compositions and Methods of Using Same
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/519,109B
 FILING DATE: 25-AUG-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-CY 1795
 TELECOMMUNICATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 10
 OTHER INFORMATION: /note= "The carboxy-terminus is a
 carboxamide."
 US-08-519-109B-26

Query Match Score 25; DB 2; Length 10;
 Best Local Similarity 44.4%; Pred. No. 3.4e+02;
 Matches 4; Conservative 2; Indels 0;
 Gaps 0;

Qy 2 ISVPLTSVP 10
 Db 2 LDVPLLDVP 10

RESULT 15
 US-08-482-228-108
 Sequence 108, Application US/08482228
 Patent No. 5966753
 GENERAL INFORMATION:
 APPLICANT: Tseng-Law, Janet
 APPLICANT: Kobori, Joan A.
 APPLICANT: Al-Abdaly, Fahad A.
 APPLICANT: Guillermo, Roy
 APPLICANT: Heigerson, Sam L.
 APPLICANT: Deans, Robert J.
 TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
 SELECTION MEDIATED BY PEPTIDE RELEASE
 NUMBER OF SEQUENCES: 215
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Janice Guthrie, Ph.D.
 STREET: P.O. Box 15210
 CITY: Irvine
 STATE: California
 COUNTRY: USA
 ZIP: 92713-5210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/492,228
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Guthrie, Janice
 REGISTRATION NUMBER: 35,170
 TELEPHONE: (714) 440-5353
 TELEFAX: (714) 553-952
 INFORMATION FOR SEQ ID NO: 108:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 US-08-482-228-108

Query Match Score 25; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;

Sun Sep 5 11:41:16 2004

us-09-761-636a-7.closed.rai

Page 7

	Matches	6;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	CISVPLTSV	9							
Db	2	CIDVFLTCV	10							

Search completed: September 5, 2004, 10:48:51
Job time : 21 secs

This Page Blank (uspto)

Run on:	September 5, 2004, 10:52:56 ; Search time 21 Seconds (without alignments)	77.869 Million cell updates/sec			
Title:	US-09-761-636A-8				
Perfect score:	100				
Sequence:	1 CAGSELGKSTNTFCCKPCC 17				
Scoring table:	BLOSUM62				
	Gapopen 10.0 , Gapext 0.5				
Searched:	283366 seqs, 96191526 residues				
Total number of hits satisfying chosen parameters:	2990				
Minimum DB seq length: 0					
Maximum DB seq length: 17					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Database :	PIR_78;*: 1: Piri;*: 2: piri2;*: 3: piri3;*: 4: Piri;*				
	Listing First 45 summaries				
	PIR_78;*: 1: Piri;*: 2: piri2;*: 3: piri3;*: 4: Piri;*				
	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
	SUMMARIES				
Result No.	Score	Query Match	Length	DB ID	Description
-	-	-	-	-	-
1	34	34.0	16	2 PH1477	T-cell receptor be
2	33.5	33.5	12	2 PH0216	T-cell receptor be
3	32	32.0	16	2 PH1472	T-cell receptor be
4	32	32.0	16	2 PH1473	T-cell receptor be
5	32	32.0	16	2 PH1480	T-cell receptor be
6	30	30.0	12	2 S47394	T-cell antigen rec
7	29.5	29.5	13	2 S47357	T-cell antigen rec
8	29	29.0	12	2 S26549	T-cell receptor be
9	29	29.0	14	2 G44957	photosystem II oxy
10	29	29.0	17	2 C24166	photosystem II ext
11	28	28.0	12	2 PH1463	T-cell receptor be
12	28	28.0	12	2 PH1466	T-cell receptor be
13	28	28.0	13	2 S47400	T-cell antigen rec
14	28	28.0	16	2 PH1474	T-cell receptor be
15	27	27.0	11	2 PT0217	T-cell receptor be
16	27	27.0	12	2 S47391	T-cell antigen rec
17	27	27.0	13	2 S47383	T-cell antigen rec
18	27	27.0	14	2 PA0013	photosystem II oxy
19	27	27.0	16	2 PH1476	T-cell receptor be
20	27	27.0	17	2 S57519	T cell receptor be
21	26	26.0	11	2 S57575	T cell receptor V-
22	26	26.0	12	2 S47395	T-cell antigen rec
23	26	26.0	13	2 S47381	T-cell antigen rec
24	26	26.0	15	2 B49655	T-cell receptor be
25	25.5	25.5	13	2 S47382	T-cell antigen rec
26	25.5	25.5	15	2 PH0752	T-cell receptor be
27	25.5	25.5	15	2 PH0750	T-cell receptor be
28	25	25.0	10	2 S23371	T-cell receptor al
29	25	25.0	11	2 PH0947	T-cell receptor be

T-cell receptor beta chain (clone A24/12.2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1472
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J.; Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; MUID:93171821; PMID:8436911
 A;Accession: PH1472
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS>
 A;Experimental source: cytolytic T-lymphocyte
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match Score 32; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CASELGKSTN 10
 Db 1 CASSGTGTTN 10

RESULT 4
 PH1473
 T-cell receptor beta chain (clone A3/IIIC5) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1473
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J.; Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; MUID:93171821; PMID:8436911
 A;Accession: PH1473
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS>
 A;Experimental source: cytolytic T-lymphocyte
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match Score 32; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CASELGKSTN 10
 Db 1 CASSGTGTTN 10

RESULT 5
 PH1480
 T-cell receptor beta chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 27-Oct-1995
 C;Accession: PH1480; PH1478
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J.; Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; MUID:93171821; PMID:8436911
 A;Accession: PH1480
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS1>
 A;Experimental source: cytolytic T-lymphocyte, clone A3/C80b
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS2>
 A;Experimental source: cytolytic T-lymphocyte, clone A24/PEFS
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match Score 32; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CASELGKSTN 10
 Db 1 CASSGTGTTN 10

RESULT 6
 S47394
 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47394; S47369
 R;Lechner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
 A;Reference number: S47355
 A;Accession: S47394
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <LEH>
 A;Cross-references: EMBL:Z35714; PIDN:CAA84783.1; PMID:9527524; EMBL:Z35694;
 C;Keywords: T-cell receptor

Query Match Score 30; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTF 12
 Db 1 CASSIGNGYTF 12

RESULT 7
 S47357
 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47357
 R;Lechner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
 A;Reference number: S47355
 A;Accession: S47357
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35681; PIDN:CAA84750.1; PMID:9527452
 C;Keywords: T-cell receptor

Query Match Score 29.5%; DB 2; Length 13;
 Best Local Similarity 63.6%; Pred. No. 2.3e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CASELGKSTNT 11
 Db 1 CASS-GRSTD 10

RESULT 8
 S26549
 T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C;Accession: S26549; S26550
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi
 J.; Exp. Med. 176, 439-447, 1992
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto
 A;Reference number: S26512; MUID:92361546; PMID:1380061
 A;Accession: S26549
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>
 A;Cross-references: EMBL:X67999

A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
 A;Accession: S2650
 A;Molecule type: mRNA
 A;Residues: 1-12 <CA2>
 A;Cross-references: EMBL:X68000
 A;Experimental source: cytolytic T-lymphocyte, clone Cw3/Casi
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 29.0%; Score 29; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CASELGK 8
 Db 1 CASSLGK 8

RESULT 9
 G44957
 photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samson NN) (fragment)
 C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993
 C;Accession: G44957
 R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
 Plant Cell 31; 215-221, 1990
 A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum
 A;Reference number: A44957
 A;Accession: G44957
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <PAK>

Query Match 29.0%; Score 29; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GKSTNTPCKP 15
 Db 3 GEAAANVFGKPK 12

RESULT 10
 C24166
 photosystem II extrinsic membrane protein - spinach (fragment)
 C;Species: Spinacia oleracea (spinach)
 C;Date: 05-Jun-1987 #sequence_revision 21-May-1988 #text_change 24-Apr-1998
 C;Accession: C24166
 R;Vater, J.; Salnikow, J.; Jansson, C.
 FEBS Lett. 203; 230-234, 1986
 A;Title: N-terminal sequence determination and secondary structure analysis of extrinsic
 A;Accession: C24166
 A;Molecule type: protein
 A;Residues: 1-17 <VAT>
 C;Superfamily: photosystem II oxygen-evolving complex protein 2
 C;Keywords: chloroplast; membrane protein; thylakoid

Query Match 29.0%; Score 29; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GKSTNTPCKP 15
 Db 2 GEAAANVFGKPK 11

RESULT 11
 PH1463
 T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1463

R;Casanova, J.L.; Martinton, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J. Exp. Med. 177; 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; PMID:93171821; PMID:8436911
 A;Molecule type: mRNA
 A;Residues: 1-12 <CS>
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 12;
 Best Local Similarity 62.3%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CASELGK 8
 Db 1 CASSLGK 8

RESULT 12
 PH1466
 T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1466
 R;Casanova, J.L.; Martinton, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J. Exp. Med. 177; 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; PMID:93171821; PMID:8436911
 A;Molecule type: mRNA
 A;Residue: 1-12 <CS>
 A;Experimental source: cytolytic T-lymphocyte
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CASELGK 7
 Db 1 CASSLGQ 7

RESULT 13
 S47400
 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47400
 R;Lechner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Accession: S47355
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross references: EMBL:235678; NID:9527535; PIDN:CAA847471; PID:9527536
 C;Keywords: T-cell receptor

Query Match 28.0%; Score 28; DB 2; Length 13;
 Best Local Similarity 41.7%; Pred. No. 5e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTF 12
 Db 1 CASSVALATEAF 12

RESULT 14

```

PH1474 receptor beta chain (clone A2/25) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1474
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatibility
A;Reference number: PH1430; MUID:33171621; PMID:8436911
A;Accession: PH1474
A;Molecule type: mRNA
A;Residues: 1-16 <CDS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match Score 28; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASELGKSTN 10
   |||| |
   1 CASSFGTGN 10

Db

RESULT 15
PT0217 receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0217
R; Nakano, N.; Kikutani, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0217
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CASELG 6
   |||| |
   1 CASRLG 6

Db

```

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.0	14	CX1A_CONBE	P58623 conus betulinus
2	26	26.0	12	PSP3_PHYPA	P80622 physcomitrium
3	25.5	25.5	15	UC19_MAIZE	P80625 zea mays (m)
4	24	24.0	15	CXA1_COINZE	P01549 conus geogr
5	23	23.0	13	CXA2_CONGE	P01550 conus geogr
6	23	23.0	13	PBBP_PINNS	P28878 conus striatus
7	23	23.0	13	CA1_CONCN	P81668 pinus pinaster
8	23	23.0	14	CA1_CONMA	P56973 conus consors
9	23	23.0	14	CA1_CONNA	P01521 conus magus
10	23	23.0	15	CX1B_CONBE	P58624 conus pennatus
11	23	23.0	15	CXA2_CONAL	P56640 conus aulicus
12	23	23.0	16	CXA1_CONAL	P56639 conus aulicus
13	23	23.0	16	CXA3_CONAL	P56661 conus aulicus
14	23	23.0	16	CXA4_CONPE	P50944 conus pennatus
15	23	23.0	16	CXAB_CONPE	P50945 conus pennatus
16	22	22.0	15	ARCA_STRPS	P58827 streptococcoides
17	22	22.0	15	NMSO_PSETE	P59073 pseudorajae
18	21	21.0	12	CXL3_CONMR	P58809 conus marmoratus
19	21	21.0	12	CXST_CONTE	P58846 conus testiculus
20	21	21.0	15	SDM_STRGR	P80733 streptomyces
21	20	20.0	12	UR2B_CATCO	P04559 catostomus
22	20	20.0	12	V23K_WSSV	P82005 white spot
23	20	20.0	13	LIGA_TRAVE	P20011 tramea leontine
24	20	20.0	14	JAPI_RANJA	P83105 rana japonica
25	19	19.0	7	TPFY_PACDA	P83457 pacynodus
26	19	19.0	7	UFO4_MOUSE	P38642 mus musculus
27	19	19.0	10	COXM_RAT	P80431 rattus norvegicus
28	19	19.0	11	CX5A_CONAL	P58848 conus aulicus
29	19	19.0	11	CX5B_CONAL	P58849 conus aulicus
30	19	19.0	12	FAR7_PENMO	P83322 penaeus japonicus
31	19	19.0	13	FARB_ASCSU	P43173 ascaris suum
32	19	19.0	15	CX3A_CONQU	P58841 conus querquedula
33	19	19.0	15	CX3B_CONQU	P58842 conus querquedula

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5						Alignments					
Searched: 141681 seqs, 52070155 residues						RESULT 1					
Total number of hits satisfying chosen parameters: 943						ID CX1A_CONBE	STANDARD;	PRT;	14 AA.		
Minimum DB seq length: 0						AC P58623;	DT 28-FEB-2003 (Rel. 41, Created)				
Maximum DB seq length: 17							DT 28-FEB-2003 (Rel. 41, Last sequence update)				
Post-processing: Minimum Match 0%							DB Conotoxin_BetXIA.				
Database : SwissProt_42;*						OS Conus betulinus (Beech cone).					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						CC -!- TISSUE-SPECIFICITY: Expressed by the venom duct.					
						CC -!- MASS SPECTROMETRY: PubMed=10591037;					
						RX Chen J.-S., Pan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.; RT "Studies on conotoxins from Conus betulinus,"; RL J. Nat. Toxins 8:341-349 (1999).					
						CC -!- SUBCELLULAR LOCATION: Secreted.					
						CC -!- TISSUE-SPECIFICITY: Belongs to the M-SUPERFAMILY OF CONOTOXINS.					
						KW Neurotoxin; Toxin.					
						FT DISURFID 1 9 PROBABLE.					
						FT DISURFID 2 12 PROBABLE.					
						FT DISURFID 6 13 PROBABLE.					
						SEQ SEQUENCE 14 AA; 1597 MW; 95B725AA93432EB1 CRC64;					
						Query Match Score 27; DB 1; Length 14; Best Local Similarity 45.5%; Pred. No. 1.BE+02; Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;					
						QY 7 KSTNTFCPKPPC 17 : Db 3 KQSCITCMCFC 13					
SUMMARIES						RESULT 2					
						ID PSP3_PHYPA	STANDARD;	PRT;	12 AA.		
						AC P80622;	DT 01-OCT-1996 (Rel. 34, Created)				
						DT 01-OCT-1996 (Rel. 34, Last sequence update)					
						DE Oxygen-evolving enhancer protein 2 (OEE2) (24 kDa subunit of oxygen evolving system of photosystem II) (Fragment).					
						OS Physcomitrella patens (Moss).					
						OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrellales.					
						NCBI_TaxID=318; [] RN SEQUENCE.					
						RP TISSUE_Protonema; MEDLINE=9129336;					

RA Kasten B., Buck F., Nuske J., Reski R.;
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
 RT plastid enzymes";
 RL Plantae 201:261-272 (1997).

CC -!- FUNCTION: May be involved in the regulation of photosystem II.
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
 CC with the photosystem II complex.

CC -!- INDUCTION: By light.

CC -!- SIMILARITY: Belongs to the psbp family.

KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
 Multigene Family.

KW Non TER 12 12 MW; 8D2B0D54D7C4DC5 CRC64;

SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C4DC5 CRC64;

Query Match 26.0%; Score 26; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 6 GKSTNTFCKP 15
 1 : | | |
 3 GBSANVFGAP 12

RESULT 3
 UG19_MAIZE STANDARD; PRT; 15 AA.
 ID UG19_MAIZE
 AC DT 01-OCT-1996 (Rel. 34, Created)
 AC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 AC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 406)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACC clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TAXID=4577; [1]

RN SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernellet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program";
 RT Theor. Appl. Genet. 93:997-1005 (1996);
 CC -!- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown
 CC protein is: 5.6, its MW is: 18.4 kDa.
 DR MaizedB; 123951; -.
 DR MaizedB; 123951; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA873779D CRC64;

Query Match 25.5%; Score 25.5; DB 1; Length 15;
 Best Local Similarity 41.7%; Pred. No. 3.5e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 6 GKSTNTF-CKPP 16
 1 : | : |||
 2 GRRYTTGGCSPP 13

RESULT 4
 CXAL_CONGE STANDARD; PRT; 15 AA.
 ID CXAL_CONGE
 AC P01579;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

DB Alpha-conotoxin GIA [Contains: Alpha-conotoxin GI (GI)].
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.

RL MEDLINE=81191854; PubMed=7014556;

CC Gray W.R., Lague F.A., Olivera B.M., Barrett J., Cruz L.J.;
 CC "Peptide toxins from Conus geographus venom.";
 CC J. Biol. Chem. 256:4734-4740 (1981).

CC -!- DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.

KW Primary and secondary structure of conotoxin GI, a neurotoxic
 tridecapeptide from a marine snail.;"

FT RT tridecapeptide from a marine snail.;"
 SQ RT tridecapeptide from a marine snail.;"
 SEQ RT tridecapeptide from a marine snail.;"
 FT RT tridecapeptide from a marine snail.;"
 RL FEBS Lett. 148:260-262 (1982).

RN [3] DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.

RP RX MEDLINE=6466616;
 RA Gray W.R., Lague F.A., Galyean R., Atherton B., Sheppard R.C.,
 Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
 Cruz L.J., Rivier J.;
 RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives.";
 RT Biochemistry 23:2796-2802 (1984).

RN [4] COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI.

RP RX MEDLINE=95034849; PubMed=7947815;

RA Han R.M., Pagan O.R., Eterovic V.A.;
 RT "The alpha-conotoxins GI and MI distinguish between the nicotinic acetylcholine receptor agonist sites while SI does not.";
 RL Biochemistry 33:14058-14063 (1994).

RN [5] PHARMACOLOGICAL CHARACTERIZATION ON MOUSE MUSCLE-DERIVED BC3H-1 CELLS AND TORPEDO ELECTRIC ORGAN.

RP RX MEDLINE=95349531; PubMed=7623764;

RA Grobe D.R., Dunn J.M., Abramson S.N.;
 RT "alpha-Conotoxins selectively inhibit one of the two acetylcholine binding sites of nicotinic receptors.";
 RT Mol. Pharmacol. 48:105-111 (1995).

RN [6] MUTAGENESIS OF ARG-9.

RP RX MEDLINE=97317090; PubMed=9174364;

RA Grebe D.R., Gray W.R., Abramson S.N.;
 RT "Determinants involved in the affinity of alpha-conotoxins GI and SI for the muscle subtype of nicotinic acetylcholine receptors.";
 RL Biochemistry 36:6469-6474 (1997).

RN [7] X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.

RP RX MEDLINE=96378624; PubMed=8784176;

RA Guddat J.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
 RT "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A resolution.";
 RT Biochemistry 35:11329-11335 (1996).

RN [8] STRUCTURE BY NMR OF GI.

RP RX MEDLINE=8935562; PubMed=2765514;

RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiochi Y., Sakakibara S.,
 RT "Solution conformation of conotoxin GI determined by 1H nuclear magnetic resonance spectroscopy and distance geometry calculations.";
 RL Biochemistry 28:4853-4860 (1989).

RN [9] STRUCTURE BY NMR OF GI.

RP RX MEDLINE=8937269; PubMed=2775719;

RA Pardi A., Gaides A., Florence J., Manicore D.;
 RT "Solution structures of alpha-conotoxin GI determined by two-dimensional NMR spectroscopy";
 RL Biochemistry 28:4549-5501 (1989).

RN [10] STRUCTURE BY NMR OF GI.

RP RX MEDLINE=88322113; PubMed=9660176;

RA Matsennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,
 RA Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;

RT Two distinct structures of alpha-conotoxin GI in aqueous solution.";

Eur. J. Biochem. 254:238-247(1998).

[11] PIR: BY NMR OF GI.

RX MEDLINE=98239743; PubMed=9571060;

RA Gehrmann J.; Alewood P.F.; Craik D.J.;

RT "Structure determination of the three disulfide bond isomers of alpha-conotoxin GI: a model for the role of disulfide bonds in structural stability.";

RT J. Mol. Biol. 278:401-415(1998).

[12] PIR: STRUCTURE BY NMR OF AN ANTITOXIC ANALOG OF GI.

RX MEDLINE=99138341; PubMed=10508392;

RA Mok K.H.; Han K.H.

RT "NMR solution conformation of an antitoxic analogue of alpha-conotoxin GI: identification of a common nicotinic acetylcholine receptor alpha(1)-subunit binding surface for small ligands and alpha-conotoxins.";

RT Biochemistry 38:11895-11904(1999).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. The higher affinity site for alpha-conotoxin GI is the alpha/delta site on mouse muscle-derived BC3H-1 receptor, and the other site (alpha/gamma site) on nicotinic receptors from Torpedo californica electric organ.

[13] PIR: SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct family.

CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.

DR PIR: A01782; NTXN2G.

DR DR; P56373; PB45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

CC FT Acetylcholine receptor inhibitor; Amidation.

DR PDB; INOT; 07-DBC-96.

DR PDB; 1XGA; 16-FEB-99.

DR PDB; 1XGB; 16-FEB-99.

DR PDB; 1XGC; 23-MAR-99.

DR PDB; 1Q3A; 06-OCT-99.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

CC FT Acetylcholine receptor inhibitor; Amidation; 3D-structure.

FT PEPTIDE 1 15 ALPHA-CONOTOXIN GIA.

FT PEPTIDE 1 15 ALPHA-CONOTOXIN GI.

FT PEPTIDE 1 13 AMIDATION (G-14 PROVIDE AMIDE GROUP) (IN

FT MOD RES 15 15 AMIDATION (IN ALPHA-CONOTOXIN GI). R->A: REDUCTION IN AFFINITY FOR BOTH

FT DISULFID 3 13 ALPHA/DELTA AND ALPHA/GAMMA SITES ON BC3H-1 RECEPTORS AND LOSS OF AFFINITY FOR BOTH ALPHA/DELTA AND ALPHA/GAMMA SITES ON TORPEDO RECEPTORS (IN GI).

FT STRAND 2 2 ALPHA-CONOTOXIN CONE

FT HELIX 5 10 ALPHA-CONOTOXIN CONE

FT STRAND 12 12 ALPHA-CONOTOXIN CONE

FT SEQUENCE 15 AA; 1628 MW; 2AE73EE90F8C2E19 CRC64;

CC Query Match Score 24; DB 1; Length 15; Best Local Similarity 60.0%; Pred. No. 6.2e+02; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC RN [1] PIR: A01783; NTXN2G.

CC DR PIR; A40312; NTXNAS.

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae;

OC Conus.

[11] NCBI_TAXID=6491;

RN [1]

RP SEQUNCE.

RX MEDLINE=81191854; PubMed=7014556;

RA Gray W.R.; Luque A.; Olivera B.M.; Barrett J.; Cruz L.J.;

RT "Peptide toxins from Conus geographus venom.";

RT J. Biol. Chem. 256:4734-4740(1981).

[12] RL RN [1]

RP DISULFIDE BONDS.

RX MEDLINE=84280842; PubMed=6466616;

RA Gray W.R.; Luque F.A.; Galvean R.; Atherton E.; Sheppard R.C.;

RT Stone B.L.; Reyes A.; Alford J.; McIntosh M.; Olivera B.M.;

RA Cruz L.J.; Rivier J.

RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives.";

RT Biochemistry 23:12796-2802(1984).

-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.

[13] CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct

CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.

CC DR PIR; A01783; NTXN2G.

DR HSSP; P56373; PB45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

CC FT Acetylcholine receptor inhibitor; Amidation.

DR PDB; DISUFID 2 7

DR PDB; DISUFID 3 13

DR PDB; MOD_RES 13 13 AMIDATION.

DR SQ SEQUENCE 13 AA; 1422 MW; DEEB31C39297ED CRC64;

CC QY Query Match Score 23; DB 1; Length 13;

CC DT Best Local Similarity 60.0%; Pred. No. 7.9e+02;

CC Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC RN [1] PIR: A01783; NTXN2G.

CC DR PIR; A40312; NTXNAS.

RESULT 6 CXAA_CONST STANDARD; PRT; 13 AA.

ID CXAA_CONST STANDARD;

AC P28578;

AC 01-DEC-1992 (Rel. 24, Created)

AC 01-DEC-1992 (Rel. 24, Last sequence update)

AC 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin STA (SIA).

OS Conus striatus (Striated cone).

OC Apogastropoda; Mollusca; Gastropoda; Orthogastropoda;

OC Neogastropoda; Conoidea; Conidae;

OC Conus.

NCBI_TAXID=6493;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=91369955; PubMed=1692838;

RA Myers R.A.; Zafarella G.C.; Gray W.R.; Abbot J.; Cruz L.J.;

RA Olivera B.M.;

RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine receptors.";

RT RT receptors.";

RL RA

RA Biochemistry 30:9370-9377(1991).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.

[14] CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct

CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.

CC DR PIR; A40312; NTXNAS.

RESULT 5 CXA2_CONGE STANDARD; PRT; 13 AA.

ID CXA2_CONGE STANDARD;

AC P01520;

AC 21-JUL-1986 (Rel. 01, Created)

AC 21-JUL-1986 (Rel. 01, Last sequence update)

AC 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin GII.

OS Conus geographus (Geography cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Conoidea; Conidae;

OC Conus.

NCBI_TAXID=6493;

RN [1]

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; DEF1931982457EBO CRC64;

Query Match 23.0%; Score 23; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 7.9e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Del 0; Cgap 0;

QY 13 CKPPC 17
Db 3 CHPAC 7

RESULT 7
PSBP_PTNPS STANDARD PRT; 13 AA.
ID PSBP_PTNPS STANDARD PRT; 13 AA.
AC P81668; DR 1B45; 09-JUL-99.
KW Postsynaptic neurotoxin; Neurotoxin; Inhibitor; Amidation.
KW Acetylcholine receptor inhibitor; Amidation.
KW 3D-structure.
DT 15-JUL-1999 (Rel. 3B, Created)
DT 15-JUL-1999 (Rel. 3B, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEB2) (23 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
GN PSSBP.
OS Pinus pinaster (Maritime pine).
OC Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647; [1]
RN SEQUENCE.
RP TISSUE_Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pilonneau C., Bauw G., Dubois C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins."
RT Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
with the photosystem II complex (By similarity).
CC -!- MISCELLANEOUS: On the 2D-gel the determined PI of this protein
(spot N179) is 5.9, its MW is: 22 kDa.
CC -!- SIMILARITY: Belongs to the psbP family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 23.0%; Score 23; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 7.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; Del 0; Cgap 0;

QY 6 GKSTNTFKCKP 15
Db 3 GEAANVFGAP 12

RESULT 8
CXAA1_CONCN STANDARD PRT; 14 AA.
ID CXAA1_CONCN STANDARD PRT; 14 AA.
AC P56973; DR 1A; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin CnIA [Contains: Alpha-conotoxin CnIB].
OS Conus consors (Singed cone).
Eukarya; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Gastropoda; Orthogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101297; [1]
RN SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
RP

DR HSSP; P56973; 1B45.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 3 8
 FT DISULFID 4 14
 MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1499 MW; DEEE9189BF5B5BD CRC64;

Query Match 23.0%; Score 23; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 2; CC
 Qy 13 CKPDC 17
 Db 4 CHPAC 8

RESULT 10
 CX1B CONBE STANDARD; PRT; 15 AA.
 AC P58674;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Conotoxin BerXB.
 OS Conus betulinus (Beech cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=200556; PubMed=10591037;
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
 RT "Studies on conotoxins of *Conus betulinus*.";
 RL J. Nat. Toxins 8:341-349(1999).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
 CC -|- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
 FT DISULFID 1 9 PROBABLE.
 FT DISULFID 2 12 PROBABLE.
 FT DISULFID 6 13 PROBABLE.
 SQ SEQUENCE 15 AA; 1650 MW; 374984F08E311337 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 9.1e+02; Indels 1; Mismatches 1; Gaps 0;
 Matches 3; Conservative 1; CC
 Qy 13 CKPDC 17
 Db 2 CELPC 6

RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D., Oliveira B.M., McIntosh J.M.; Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release. " [2]
 RN STRUCTURE BY NMR.
 RX MEDLINE=20187585; PubMed=10722709;
 RA Rao J.H., Mok K.H., Oliveira B.M., McIntosh J.M., Park K.H., Han K.H.; Nuclear magnetic resonance solution conformation of alpha-conotoxin AuIB acetylcholine receptor antagonist. " [3]
 RN RP STRUCTURE BY NMR.
 RX MEDLINE=22359066; PubMed=12376538;
 RA Dutton J.L., Bansal P.S., Hogg R.C., Adams D.J., Alewood P.F., Craik D.J.; RT "A new level of conotoxin diversity, a non-native disulfide bond connectivity in alpha-conotoxin AuIB reduces structural definition but increases biological activity." [4]
 RL J. Biol. Chem. 277:48849-48857(2002).
 CC -|- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. This Peptide blocks mammalian nicotinic acetylcholine receptors composed of alpha-3/beta-4 subunits.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.
 CC -|- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.
 CC DR PDB; 1DG2; 23-MAY-00.
 DR PDB; 1MXN; 30-DEC-02.
 DR PDB; 1MXP; 30-DEC-02.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 15 AMIDATION.
 FT MOD_RES 15 15 AMIDATION.
 SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02; Indels 0; Mismatches 0; Gaps 0;
 Matches 3; Conservative 0; CC
 Qy 15 PPC 17
 Db 6 PPC 8

RESULT 12
 CXA1_CONAL STANDARD; ERT; 16 AA.
 AC P566379;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE Alpha-conotoxin AuIA.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
 OC NCBI_TaxID=89437;
 RN [1] SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D., Oliveira B.M., McIntosh J.M.; Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release. " [2]
 RN J. Neurosci. 18:8571-8579(1998).
 CC -|- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. This peptide blocks mammalian nicotinic acetylcholine receptors composed of alpha-3/beta-4 subunits.

-|- SUBCELLULAR LOCATION: Secreted.

-|- TISSUE SPECIFICITY: Expressed by the venom duct.

-|- MASS SPECTROMETRY: MW=175.6; METIONINE=Electrospray.

-|- SIMILARITY: Belongs to the conotoxin A-supertfamily. Alpha-type Family.

PIR: A59045; A59045.

HSSP: P50984; 1PEN.

Post-synaptic nicotinic neurotoxin; Neurotoxin; Toxin; Acetylcholine receptor inhibitor; Amidation.

FT DISULFID 2 8

FT DISULFID 3 16

FT MOD RES 16 16 AMIDATION.

SQ SEQUENCE 16 AA; 1731 MW; 1E310FB8BFDC7001 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Gapless 0.

Qy 15 PPC 17
|||
6 PPC 8

RESULT 13

CXAA	CONAL	STANDARD;	PRT;	16 AA.
CXAA	CXAA CONAL			
AC	P56641;			
DT	DT 15-DEC-1998 (Rel. 37, Created)			
DT	DT 15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DB	Alpha-conotoxin AuIC.			
OS	Osmerus eperlanus (Court cone)			
OC	Bukaryote; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastrropoda; Neogastropoda; Conoidea; Conidae; Coronus.			
OX	NCBI_TaxID=89437;			
RN	RN			
RP	RP			
RC	RC			
TISSUE-Venom;				
RX	Medline:99033929; PubMed:9786965;			
RA	Iluo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D., Olivera B.M., McIntosh J.M.;			
RA	"Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release J. Neurosci. 18:8871-8879 (1998).			
RT	- FUNCTION: Alpha-conotoxins act on post-synaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. This peptide blocks mammalian nicotinic acetylcholine receptors composed of alpha-3/beta-4 subunits.			
CC	- - SUBCELLULAR LOCATION: Secreted.			
CC	- - TISSUE SPECIFICITY: Expressed by the venom duct.			
CC	- - MASS SPECTROMETRY: MW=1667.6; METIONINE=Electrospray.			
CC	- - SIMILARITY: Belongs to the conotoxin A-supertfamily. Alpha-type family.			
CC	PIR: C59045; C59045.			
DR	DR; C59045; 1PEN.			
KW	Post-synaptic neurotoxin; Neurotoxin; Toxin;			
KW	Acetylcholine receptor inhibitor; Amidation.			
FT	DISULFID 2 8			
FT	DISULFID 3 16			
FT	MOD RES 16 16 AMIDATION.			
SQ	SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;			

Query Match 23.0%; Score 23; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Gapless 0.

Qy 15 PPC 17
|||
6 PPC 8

RESULT 15

CXAB_CONPE	STANDARD;	PRT;	16 AA.
AC			
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Alpha-conotoxin PnIB.		
OS	Conus pennaceus (Feathered cone).		
OC	Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;		
OC	Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;		
OC	Neogastropoda; Conoidea; Conidae; Conus.		
OX	NCBI_TaxID=37335;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE-VENOM;		
RX	MEDLINE=94347719; PubMed=8068627;		
RA	Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,		
RA	Spira M.E., Zlotkin E.;		
RT	"New mollusc-specific alpha-conotoxins block Aplyisia neuronal acetylcholine receptors."		
RL	Biochemistry 33:9523-9529(1994).		
RN	[2]		
RP	SULFATION OF TYR-15.		
RX	MEDLINE=99242956; PubMed=10226369;		
RA	Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M., Baldwin M.A., Burlingame A.L.,		
RA	"Identification of tyrosine sulfation in Conus pennaceus conotoxins alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and phosphopeptides by electrospray, matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass spectrometry";		
RL	J. Mass Spectrom. 34:447-454 (1999).		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).		
RX	MEDLINE=9744322; PubMed=929851;		
RA	Hu S.H., Gehrmann J., Alswood P.F., Craik D.J., Martin J.L.;		
RT	"Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB: Comparison with alpha-conotoxins PnIA and GI.";		
RL	Biochemistry 36:11323-11330(1997).		
CC	-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. In contrast to other alpha-conotoxins, which are selective for vertebrate skeletal muscle nAChR, the Conus pennaceus alpha-conotoxins block nAChR in mollusks.		
CC	-!- SUBCELLULAR LOCATION: Secreted.		
CC	-!- TISSUE SPECIFICITY: Expressed by the venom duct.		
CC	-!- SIMILARITY: Belongs to the conotoxin A-supertfamily. Alpha-type family.		
DR	PIR: B54377; B54877.		
KW	Possynaptic neurotoxin; Neurotoxin; Toxin;		
KW	Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.		
FT	DISULFID 2 8		
FT	DISULFID 3 16		
FT	MOD RES 15 15		
FT	MOD RES 16 16		
FT	HELIX 2 4		
FT	HELIX 6 11		
FT	TURN 13 16		
SQ	SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;		
Query Match	23.0%	Score 23;	DB 1;
Best Local Similarity	100.0%	Length 16;	
Matches 3;	Conservative 0;	Pred. No. 9.7e+02;	
Matches 3;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	15 PPC 17		
Db	6 PPC 8		

This Page Blank (uspto)

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.0	13	Q8QG25	08qg25 fugu rubripes
2	26	26.0	13	Q918U6	Q918U6 human papilloma virus
3	26	26.0	13	Q918T4	Q918T4 human papilloma virus
4	26	26.0	13	Q918T6	Q918T6 human papilloma virus
5	26	26.0	16	Q918U2	Q918U2 human papilloma virus
6	26	26.0	16	Q918T1	Q918T1 human papilloma virus
7	26	26.0	16	Q918U8	Q918U8 human papilloma virus
8	26	26.0	16	Q918U4	Q918U4 human papilloma virus
9	26	26.0	16	Q918T9	Q918T9 human papilloma virus
10	26	26.0	17	Q9C0S9	Q9C0S9 claviceps purpurea
11	26	26.0	17	Q9C0S6	Q9C0S6 claviceps purpurea
12	26	26.0	17	Q8N1U7	Q8N1U7 fusarium sojae
13	26	26.0	17	Q9C1U6	Q9C1U6 fusarium sojae
14	26	26.0	17	Q9C0S7	Q9C0S7 claviceps purpurea
15	26	26.0	17	Q9C0S8	Q9C0S8 claviceps purpurea
16	26	26.0	17	Q9C1Q8	Q9C1Q8 claviceps purpurea

[1] Sequence from N.A.
 RP STRAIN=HPV16E2CC1;
 RC "Sequence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF407214; AAL01388.1;
 FT NON-TER
 SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match Score 26; DB 12; Length 16;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

RESULT 7
 Q918U6 PRELIMINARY; PRT; 16 AA.
 AC Q918U6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE E1 protein (Fragment).
 GN RN [1]
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E2CC1;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF407215; AAL01391.1;
 FT NON-TER
 SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match Score 26; DB 12; Length 16;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

RESULT 8
 Q918U4 PRELIMINARY; PRT; 16 AA.
 AC Q918U4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE E1 protein (Fragment).
 GN RN [1]
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E2CC1;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human Papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.


```

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Cjap-2, and Cjap-4;
RC Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA Kuldau G.A.;
RT "Characterization of Claviceps species pathogenic on sorghum by
sequence analysis of the beta-tubulin gene intron 3 region and EF1-
alpha gene intron 4."
RT Mycologia 93:541-551 (2001).
RL AF255894; AAK37639.1;
DR EMBL; AF255894; AAK37639.1;
DR EMBL; AF255895; AAK37640.1;
FT NON-TER 1 1
FT NON-TER 17 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match 26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ASELGKST 9
Db 8 AAELGKGS 15

RESULT 15
Q9COS8 PRELIMINARY; PRT; 17 AA.
ID Q9COS8
AC Q9COS8;
DT 01-JUN-2001 (TREMBUREL. 17, Created)
DT 01-JUN-2001 (TREMBUREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMBUREL. 17, Last annotation update)
DB EF1-alpha (Fragment)
GN TEF1.
OS Claviceps paspali (paspalum stagers ergot).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OC NCBTAXID=40601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cpas-L, and Cpas-2;
RA Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA Kuldau G.A.;
RT "Characterization of Claviceps species pathogenic on sorghum by
sequence analysis of the beta-tubulin gene intron 3 region and EF1-
alpha gene intron 4."
RT Mycologia 93:541-551 (2001).
RL AF255892; AAK37637.1;
DR EMBL; AF255893; AAK37638.1;
FT NON-TER 1 1
FT NON-TER 17 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match 26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ASELGKST 9
Db 8 AAELGKGS 15

```

Search completed: September 5, 2004, 10:56:03
Job time : 58 secs

This Page Blank (uspto)

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	17	4	AAU04527	Aau04527 VEGF base
2	97	97.0	17	4	AAU04550	Aau04550 VEGF base
3	97	97.0	17	4	AAU04546	Aau04546 VEGF base
4	93	93.0	17	4	AAU04547	Aau04547 VEGF base
5	93	93.0	17	4	AAU04551	Aau04551 VEGF base
6	93	93.0	17	4	AAU04549	Aau04549 VEGF base
7	89	89.0	17	4	AAU04548	Aau04548 VEGF base
8	72	72.0	13	4	AAU04524	Aau04524 VEGF base
9	69	69.0	13	4	AAU04534	Aau04534 VEGF base
10	65	65.0	13	4	AAU04535	Aau04535 VEGF base
11	65	65.0	13	4	AAU04537	Aau04537 VEGF base
12	61	61.0	13	4	AAU04536	Aau04536 VEGF base
13	48	48.0	14	4	AAU04542	Peptide #
14	39	39.0	8	4	AAU048481	Aau048481 Peptide #
15	37	37.0	10	2	AAW0122	Human ago
16	37	37.0	12	3	AYA57039	Feline im
17	35	35.0	17	3	AYA33529	PKC sequ
18	33	33.0	16	3	AYA93529	Aay93529 Human ser
19	32	32.0	9	4	AAB98568	Aab98568 Human TAD
20	32	32.0	11	4	AAB46652	Aab46652 HIV-1 Tat
21	32	32.0	12	2	AAR43828	Aar43828 HIV-1 Tat
22	32	32.0	12	2	Aaw11133	Aaw11133 HIV-1 Tat
23	32	32.0	12	2	AANW2574	Aaw52574 Cyclic pe
24	32	32.0	12	2	AYA24778	Aay24778 HIV-1 Tat
25	32	32.0	12	2	AYA17381	Aay17381 Antimicro

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Database : A_Geneseq_29Jan01:*

1: GeneseqP_980s:*

2: GeneseqP_1990s:*

3: GeneseqP_200s:*

4: GeneseqP_2001s:*

5: GeneseqP_2002s:*

6: GeneseqP_2003ab:*

7: GeneseqP_2003bc:*

8: GeneseqP_2004s:*

Total number of hits satisfying chosen parameters: 470470

Minimum DB seq length: 0
Maximum DB seq length: 17

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

ID AAU04527 standard; protein; 17 AA.

XX AAU04527;

XX DT 26-SEP-2001 (first entry)

XX DB VEGF based bicyclic dimeric peptide #1.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
XX KW Synthetic.

XX FH Key Disulfide-bond 1.13 /note= "This bond cyclises the peptide"

FT FT Disulfide-bond 1.7 /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide, or to residue 1 of the sequence appearing as AAU04528, also forming a dimeric peptide".
XX PN WO200152875-A1.
XX PD 26-JUL-2001.
XX PA (LUDW-) LUDMIG INST CANCER RES.
XX PF 18-JAN-2001; 2001WO-US0001533.
XX PI Achen MG, Hughes RA, Stecker S, Cendron A;
XX PR 18-JAN-2000; 2000US-017623P.
XX PR 16-MAY-2000; 2000US-0204530P.
XX XX

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
XX PT
XX PS Claim 59; Page 32; 102pp; English.

CC peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

XX Sequence 17 AA;

Query Match Score 93; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.e-07;
Matches 15; Conservative 2; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFKPKPC 17
|||:|||:|||:|||:
Db 1 CASELGRSTNSFKPKPC 17

RESULT 7
AAU04548

ID AAU04548 standard; peptide; 17 AA.

XX AAU04548;

XX 26-SEP-2001 (first entry)

DB VEGF based bicyclic dimeric Peptide #5.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;

KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1.-13
/note= "This bond cyclises the peptide"

FT Disulfide-bond 17
/note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide"

XX WO200152075-A1.

XX 26-JUL-2001.

XX P1 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX DR 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment

CC from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX Example 26; Page 49; 102pp; English.

PT PT
PS PS
XX The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic Peptide by a measuring beta-carbon separation on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a Growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

XX Sequence 17 AA;

Query Match Score 89; DB 4; Length 17;
Best Local Similarity 89.0%; Pred. No. 2.7e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFKPKPC 17
|||:|||:|||:
Db 1 CASDVGKSTNTWKPKPC 17

RESULT 8

AAU04524

ID AAU04524 standard; peptide; 13 AA.

XX AAU04524;

AC AC

DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic Peptide 1.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

XX KW KW
KW neovascularisation; lymphangiogenesis; psoriasis; tumour; KW diabetes induced neovascular sequelae; rheumatoid arthritis; KW diabetic retinopathy; chronic inflammation; cyclic.

OS OS

XX Key Location/Qualifiers
FT Disulfide-bond 1..13
FT /note= "This bond cyclises the peptide"
FT Disulfide-bond 1
FT /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide"

XX PN WO200152075-A1.
XX PD 26-JUL-2001.
XX P1 18-JAN-2001; 2001WO-US001533.
XX PR 18-JAN-2000; 2000US-0176293P.
XX PR 16-MAY-2000; 2000US-0204590P.
PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX DR 2001-442248/47.
XX PP 18-JAN-2001; 2001WO-US001533.
XX PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.

XX XX WO200152875-A1.
 PA PN
 XX XX 26-JUL-2001.
 PI PD
 XX PF
 DR 18-JAN-2001; 2001WO-US001533.
 XX PR
 PT 18-JAN-2000; 2000US-0176293P.
 PT PR
 PT 16-MAY-2000; 2000US-0204590P.
 PT XX (LUDW-) LUDWIG INST CANCER RES.
 PR PA
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 PS XX
 XX PI WPI: 2001-442248/47.
 PS English.
 XX Example 25; Page 47; 102pp; English.
 CC Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 CC or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 CC from an exposed loop of a growth factor protein by oxidizing the cysteine
 residues.
 CC XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX Sequence 13 AA;
 CC Query Match 72.0%; Score 72; DB 4; Length 13;
 CC Best Local Similarity 100.0%; Pred. No. 0.00073;
 CC Matches 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13
 SQ Sequence 13 AA;
 CC Query Match 69.0%; Score 69; DB 4; Length 13;
 CC Best Local Similarity 92.3%; Pred. No. 0.002;
 CC Matches 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13
 DT 26-SEP-2001 (first entry)
 RESULT 10
 AAU04535
 ID AAU04533 standard; peptide; 13 AA.
 AC AAU04534;
 XX
 DT 26-SEP-2001 (first entry)
 XX VEGF based monocyclic peptide 12.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 XX DE VEGF based monocyclic peptide 13.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 FT /note= "This bond cyclises the peptide"
 FT

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 Key Disulfide-bond 1..13
 /note= "This bond cyclises the peptide"
 PN WO200152875-A1.
 PD 26-JUL-2001.
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX DR 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX PS Example 25; Page 47; 102pp; English.
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, Psoriasis, arthropathy,
 CC hemangoma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX Sequence 13 AA;
 Query Match 65.0%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.008;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13
 SQ Sequence 13 AA;

ID AAU04537 standard; peptide; 13 AA.
 XX
 AC AAU04537;
 XX DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 15.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumor;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX OS Synthet.
 XX PH Location/Qualifiers
 /note= "This bond cyclises the peptide"
 XX Key Location/Qualifiers
 FT Disulfide-bond 1..13
 /note= "This bond cyclises the peptide"
 XX PR 18-JAN-2001; 2000WO-US00152875-A1.
 PR 16-MAY-2000; 2000US-0204590P.
 PR 18-JUN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX DR 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the Cysteine
 PT residues.
 XX PS Example 25; Page 47; 102pp; English.
 XX The sequence represents monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, Psoriasis, arthropathy,
 CC hemangoma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX Sequence 13 AA;
 Query Match 65.0%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.008;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13
 SQ Sequence 13 AA;

Query Match 65.0%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.008;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13
 SQ Sequence 13 AA;

RESULT 11
 AAU04537

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 13 AA:

Query 1 CASELGRKSTNTFC 13

Best Local Similarity 61.0%; Score 61; DB 4; Length 13;

ID AAU04536 standard; peptide; 13 AA.

XX AAU04536;

AC AAU04536;

XX DT 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 14.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS

XX FH Key Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT XX WO200152875-A1.

PN XX PD 26-JUL-2001.

PP XX P1 Achen MG, Hughes RA, Stackler S, Cendron A;

XX DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment PR from an exposed loop of a growth factor protein by oxidizing the cysteine XX residues.

PA (LUDWIG INST CANCER RES.

XX P1 Achen MG, Hughes RA, Stackler S, Cendron A;

XX DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment PR from an exposed loop of a growth factor protein by oxidizing the cysteine XX residues.

PS Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention, CC whose 3-dimensional structure is modelled on the expose loop of human CC VEGP (vascular endothelial growth factor). The invention relates to a CC method of producing a monomeric monocyclic peptide by a measuring beta- CC beta carbon separation distances on opposite antiparallel strands of a CC peptide loop fragment from an exposed loop of a growth factor protein and CC cyclising the peptide by oxidising the cysteine residues. The monocyclic CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic CC peptides) and a cyclic peptide with at least one amino acid deleted prior CC to cyclisation are used to interfere with angiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy, CC haemangoma, vascularised malignant or benign tumour, post-recovery CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold CC trauma, substance-induced neovascularisation of the liver, excessive CC hormone-related angiogenic dysfunction, diabetes induced neovascular CC sequelae, hypertension induced neovascular sequelae, or chronic liver CC infection. The peptides are also used to modulate vascular permeability CC in a mammal (the mammal has a condition characterised by fluid CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, CC or brain. The peptides are used to image blood vessels and lymphatic CC vasculature. The monomeric and bicyclic peptides are used to interfere CC

Query 1 CASELGRKSTNTFC 13

Best Local Similarity 76.9%; Score 61; DB 4; Length 13;

ID AAU04536 standard; peptide; 14 AA.

XX AAU04536;

AC AAU04536;

XX DT 21-NOV-2001 (first entry)

DE Peptide #4 inhibiting human VEGF-C mediated activation of VEGFR-3.

XX DE Human; vascular endothelial growth factor; VEGF-C; vasculogenesis; KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis; KW age-related macular degeneration; rheumatoid arthritis; cardiovascular; KW VEGFR-3.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT FT Misc-difference 11..13/
 /note= "Any amino acid"

XX PN WO200162942-A2.

XX PD 30-AUG-2001.

XX P1 Alitalo K, Jeltsch MM;

XX DR WPI; 2001-53640/59.

XX 26-FEB-2001; 2001WO-US006113.

XX PR 25-FEB-2000; 2000US-0185205P.

XX PR 18-MAY-2000; 2000US-0205331P.

XX PA (LUDWIG INST CANCER RES.

XX PA (LICN) LICENTIA OY.

XX PI Alitalo K, Jeltsch MM.

XX PS Claim 65; Page 147; 26pp; English.

XX CC The present invention relates to polypeptides that bind cellular CC receptors for vascular endothelial growth factors (VEGFs), the CC polynucleotides encoding them, and their use for identifying agents that CC modulate interactions between VEGFs and their receptors. VEGFs and their CC receptors play an important role in vasculogenesis, the development of CC the embryonic vasculature from early differentiating endothelial cells CC and angiogenesis, the process of forming new blood vessels from pre-existing ones. Modulators of interactions between VEGFs and its receptors CC may be used to treat dysfunction of the endothelial cell regulatory CC system. Such disorders include cancers, abnormal angiogenesis, CC proliferative retinopathies, age-related macular degeneration, rheumatoid CC arthritis and psoriasis. The polypeptides of the invention exhibit unique CC receptor binding profiles compared to known naturally occurring VEGFs. CC AAU0479-AAU0483 represents peptides which inhibit human VEGF-C mediated CC activation of VEGFR-3

XX SQ Sequence 14 AA;
 Query Match Best Local Similarity 48.0%; Score 48; DB 4; Length 14;
 Matches 8; Conservative 88.9%; Pred. No. 3;
 Mismatches 0; Indels 1; Gaps 0;
 RESULT 15
 ID AAW10122 standard; protein; 10 AA.
 XX AC AAW10122;
 XX DT 18-SEP-1997 (first entry)
 DE Human agouti signalling protein fragment #10.
 XX KW Agouti signalling Protein; ASP; depigmenting activity; cosmetic;
 KW hyperpigmentary condition; melasma photoageing spots; solar keratosis;
 KW post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
 KW vitiligo; leucoderma; albinism; hair greying.
 XX OS Homo sapiens.
 XX PN WO9700892-A2.
 XX PD 09-JAN-1997.
 XX PF 21-JUN-1996; 96WO-US010695.
 XX PR 23-JUN-1995; 95US-0000436P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Hearing VJ;
 XX DR WPI; 1997-087323/08.
 XX PT New agouti signal protein peptide(s) and nucleic acids - used for
 PT altering melanin prodn. for treating e.g. melasma photo-ageing spots,
 PT solar keratosis or vitiligo.
 XX MX Claim 26; Page 12; 67pp; English.
 XX CC The sequences given in AAW10101-29 are biologically active peptides and
 CC fragments of the agouti signalling protein (ASP) which have depigmenting
 CC activity. These peptides are useful for cosmetic purposes and for
 CC clinical application in the prevention or treatment of various
 CC hyperpigmentary conditions and diseases such as melasma photoageing
 CC spots, solar keratosis, and post-inflammatory hyperpigmentation such as
 CC occurs at sites of wound healing. They can also be used to provide
 CC enhanced eumelanogenesis for treating e.g. vitiligo, leucoderma, some
 CC forms of albinism and hair greying.
 XX SQ Sequence 10 AA;
 Query Match Best Local Similarity 37.0%; Score 37; DB 2; Length 10;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 8 STNTFCCKPP 16
 :||| |||
 Db 1 ATNDSCCKPP 9
 Search completed: September 5, 2004, 10:54:38
 Job time : 63 secs

XX SQ Sequence 8 AA;
 Query Match Best Local Similarity 39.0%; Score 39; DB 4; Length 8;
 Matches 7; Conservative 87.5%; Pred. No. 1.e+06;
 Mismatches 0; Indels 1; Gaps 0;

QY 9 TNTFCKPP 16

This Page Blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw mode

Run on: September 5, 2004, 10:55:07 ; Search time 66 Seconds
 (without alignments)

Scoring table: BLOSUM62

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCKPPC 17

Minimum DB seq length: 0

Maximum DB seq length: 17

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 230634

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/podata/2/pubpa/us07_pubcom.pep:
 2: /cgn2_6/podata/2/pubpa/pct_new_pub.pep:
 3: /cgn2_6/podata/2/pubpa/us06_pub.dep:
 4: /cgn2_6/podata/2/pubpa/us06_pubcom.dep:
 5: /cgn2_6/podata/2/pubpa/us07_pubcom.dep:
 6: /cgn2_6/podata/2/pubpa/pctus_pubcom.dep:
 7: /cgn2_6/podata/2/pubpa/us08_pub.dep:
 8: /cgn2_6/podata/2/pubpa/us08_pubcom.dep:
 9: /cgn2_6/podata/2/pubpa/us09_pubcom.dep:
 10: /cgn2_6/podata/2/pubpa/us09b_pubcom.dep:
 11: /cgn2_6/podata/2/pubpa/us09c_pubcom.dep:
 12: /cgn2_6/podata/2/pubpa/us09_pub.com.dep:
 13: /cgn2_6/podata/2/pubpa/us10a_pubcom.dep:
 14: /cgn2_6/podata/2/pubpa/us10b_pubcom.dep:
 15: /cgn2_6/podata/2/pubpa/us10c_pubcom.dep:
 16: /cgn2_6/podata/2/pubpa/us10_new_pub.dep:
 17: /cgn2_6/podata/2/pubpa/us60_pubcom.dep:
 18: /cgn2_6/podata/2/pubpa/us60_pubcom.dep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	100	100	17	US-09-761-636A-8
2	97	97	17	US-09-761-636A-27
3	97	97	17	US-09-761-636A-31
4	93	93	17	US-09-761-636A-28
5	93	93	17	US-09-761-636A-40
6	93	93	17	US-09-761-636A-32
7	89	89	17	US-09-761-636A-17
8	72	72	13	US-09-761-636A-29
9	69	69	13	US-09-761-636A-5
10	65	65	13	US-09-761-636A-15
11	65	65	13	US-09-761-636A-16
12	61	61	13	US-09-761-636A-18
13	37	37	10	US-10-435-238-22
14	32	32	7	US-09-805-761-61
15	32	32	7	US-09-805-761-63

Sequence 78, App1
 Sequence 4, App1
 Sequence 4, App1
 Sequence 141, App1
 Sequence 14, App1
 Sequence 454, App1
 Sequence 115, App1
 Sequence 156, App1
 Sequence 461, App1
 Sequence 21, App1
 Sequence 58, App1
 Sequence 58, App1
 Sequence 67, App1
 Sequence 4, App1
 Sequence 35, App1
 Sequence 11, App1
 Sequence 14, App1
 Sequence 335, App1
 Sequence 10, App1
 Sequence 9, App1
 Sequence 9, App1
 Sequence 9, App1
 Sequence 38, App1
 Sequence 9, App1
 Sequence 33, App1
 Sequence 104, App1

ALIGNMENTS

RESULT 1
 US-09-761-636A-8
 ; Sequence 8, Application US/09761636A
 ; GENERAL INFORMATION:
 ; Patent No. US2002006518A1
 ; APPLICANT: ACHEN, Marc
 ; APPLICANT: STACKER, Steven
 ; APPLICANT: HUGHES, Richard
 ; APPLICANT: CENDRON, Angela
 ; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 ; FILE REFERENCE: 1064_A8505 Achen et al
 ; CURRENT APPLICATION NUMBER: US 60/176,293
 ; PRIORITY FILING DATE: 2001-01-18
 ; PRIORITY APPLICATION NUMBER: US 60/176,293
 ; PRIORITY FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-761-636A-8

Query Match Best Local Similarity 100.0%; Score 100; DB 9; Length 17;
 Matches 17, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFCKPPC 17
 Db 1 CASELGKSTNTFCKPPC 17

RESULT 2
 US-09-761-636A-27
 ; Sequence 27, Application US/09761636A
 ; Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

PRIOR FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 27

LENGTH: 17

TYPE: PRT

ORGANISM: synthetic construct

US-09-761-636A-27

Query Match Score 97; DB 9; Length 17;

Best Local Similarity 94.1%; Pred. No. 9.2e-08;

Matches 16; Conservative 1; Mismatches 0;

Indels 0; Gaps 0;

RESULT 5

1 CASELGKSTNTFCCKPPC 17

||:|||||:|||||:|||||

Db 1 CASELGKSTNTFCCKPPC 17

US-09-761-636A-30

Sequence 30, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

PRIOR FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 30

LENGTH: 17

TYPE: PRT

ORGANISM: synthetic construct

US-09-761-636A-30

Query Match Score 93; DB 9; Length 17;

Best Local Similarity 88.2%; Pred. No. 3.7e-07;

Matches 15; Conservative 2; Mismatches 0;

Indels 0; Gaps 0;

RESULT 6

1 CASELGKSTNTFCCKPPC 17

||:|||||:|||||:|||||

Db 1 CASELGKSTNTFCCKPPC 17

US-09-761-636A-32

Sequence 32, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

PRIOR FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 31

LENGTH: 17

TYPE: PRT

ORGANISM: synthetic construct

US-09-761-636A-31

Query Match Score 97.0%; DB 9; Length 17;

Best Local Similarity 94.1%; Pred. No. 9.2e-08;

Matches 16; Conservative 1; Mismatches 0;

Indels 0; Gaps 0;

RESULT 4

1 CASELGKSTNTFCCKPPC 17

||:|||||:|||||:|||||

Db 1 CASELGKSTNTFCCKPPC 17

US-09-761-636A-28

Sequence 28, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

PRIOR FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

```

; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32

Query Match 93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFKCKPPC 17
Db 1 CASELGKSTNSFKCKPPC 17

RESULT 9
US-09-761-636A-15
Sequence 15, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al.
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match 69.0%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFKCKPPC 13
Db 1 CASELGKSTNTFC 13

RESULT 10
US-09-761-636A-16
Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al.
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

Query Match 89.0%; Score 89; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.5e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFKCKPPC 17
Db 1 CASDVGKSTNTWCKPPC 17

RESULT 8
US-09-761-636A-5
Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al.
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

```

Query Match 65.0%; Score 65; DB 9; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.0049; Indels 0; Gaps 0;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-09-761-636A-18
 Sequence 18, Application US/09761636A
 Patent No. US20020065218A1

GENERAL INFORMATION:
 APPLICANT: ACHEN, Marc
 APPLICANT: STACKER, Steven
 APPLICANT: HUGHES, Richard
 APPLICANT: CENDRON, Angela
 TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 FILE REFERENCE: 1064/48505 Achen et al
 CURRENT APPLICATION NUMBER: US/09/761,436A
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 60/176,293
 PRIOR FILING DATE: 2000-01-18
 PRIOR APPLICATION NUMBER: US 60/204,590
 PRIOR FILING DATE: 2000-05-16
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 18
 LENGTH: 13
 TYPE: PRT
 ORGANISM: synthetic construct
 US-09-761-636A-18

Query Match 65.0%; Score 65; DB 9; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.0049; Indels 0; Gaps 0;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13

RESULT 12
 US-09-761-636A-17
 Sequence 17, Application US/09761636A
 Patent No. US20020065218A1

GENERAL INFORMATION:
 APPLICANT: ACHEN, Marc
 APPLICANT: STACKER, Steven
 APPLICANT: HUGHES, Richard
 APPLICANT: CENDRON, Angela
 TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 FILE REFERENCE: 1064/4505 Achen et al
 CURRENT APPLICATION NUMBER: US/09/761,636A
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 60/176,293
 PRIOR FILING DATE: 2000-01-18
 PRIOR APPLICATION NUMBER: US 60/204,590
 PRIOR FILING DATE: 2000-05-16
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 17
 LENGTH: 13
 TYPE: PRT
 ORGANISM: synthetic construct
 US-09-761-636A-17

Query Match 61.0%; Score 61; DB 9; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.02; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13

RESULT 13
 US-10-435-238-22
 Sequence 22, Application US/10435238
 Publication No. US20030224972A1

GENERAL INFORMATION:
 APPLICANT: HEARING, Vincent J., JR.
 TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Protein and Peptides Thereof
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Needle & Rosenberg, P.C.
 STREET: 127 Peachtree St., N.E.
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30303-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/435,238
 FILING DATE: 08-May-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/983,157
 FILING DATE: 22-Dec-1997
 APPLICATION NUMBER: PCT/US96/10695
 FILING DATE: 21-JUN-1996
 APPLICATION NUMBER: 60/ 000,436
 FILING DATE: 23-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Spratt, Gwendolyn D.
 REGISTRATION NUMBER: 36,016
 REPERIENCE/DOCKET NUMBER: 14014.0195
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 688-0770
 TELEX/FAX: (404) 688-9880
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-10-435-238-22

Query Match 37.0%; Score 37; DB 12; Length 10;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 STNTFCKPP 16
 Db 1 ATNDSCKPP 9

RESULT 14
 US-09-805-761-61
 Sequence 61, Application US/09805761
 Patent No. US20010165174A1

GENERAL INFORMATION:
 APPLICANT: Gill, Parkesh
 APPLICANT: Masood, Rizwan
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE OLIGONUCLEOTIDES
 TITLE OF INVENTION: VEGF OLIGONUCLEOTIDES
 FILE REFERENCE: 21327-701CON2

```

; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/015,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-761-61

```

```

Query Match          Score 32; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy    9 TNTFCKP 15
      ||||| |
Db     1 TNTFFKP 7

```

```

RESULT 15
US-09-805-761-63
; Sequence 63, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 213327.701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-761-63

```

```

Query Match          Score 32; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy    9 TNTFCKP 15
      ||||| |
Db     1 TNTFFKP 7

```

Search completed: September 5, 2004, 11:01:34
Job time : 67 secs

This Page Blank (uspto)

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:53:36 ; Search time 20 Seconds
(without alignments)

43.882 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCRKP C 17

Scoring table: BL03DM2

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 157007

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5a_COMB_pep:*

2: /cgn2_6/ptodata/2/iaa/5b_COMB_pep:*

3: /cgn2_6/ptodata/2/iaa/6a_COMB_pep:*

4: /cgn2_6/ptodata/2/iaa/6b_COMB_pep:*

5: /cgn2_6/ptodata/2/iaa/PCUTS_COMB_pep:*

6: /cgn2_6/ptodata/2/iaa/backfile1_COMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	37	10 4	US-09-983-157B-22	Sequence 22, Appl		
2	32	32 0	9 4	US-09-644-600-78	Sequence 78, Appl	
3	32	32 0	9 4	US-09-554-600A-78	Sequence 78, Appl	
4	32	32 0	12 1	US-09-053-079A-4	Sequence 4, Appl	
5	32	32 0	12 2	US-08-685-589A-228	Sequence 228, Appl	
6	32	32 0	12 4	US-09-162-118-4	Sequence 4, Appl	
7	32	32 0	16 1	US-08-369-666-1	Sequence 1, Appl	
8	31	31 0	10 4	US-08-983-157B-21	Sequence 21, Appl	
9	31	31 0	16 3	US-09-328-001-4	Sequence 4, Appl	
10	31	31 0	16 4	US-09-777-010A-4	Sequence 4, Appl	
11	31	31 0	17 3	US-08-882-046-9	Sequence 9, Appl	
12	31	31 0	17 4	US-09-252-186-19	Sequence 19, Appl	
13	30	30 0	14 2	US-08-443-065B-9	Sequence 9, Appl	
14	30	30 0	14 2	US-08-425-989B-9	Sequence 9, Appl	
15	30	30 0	14 2	US-08-443-066B-9	Sequence 9, Appl	
16	30	30 0	14 3	US-08-853-010-3	Sequence 3, Appl	
17	30	30 0	14 4	US-09-148-712-13	Sequence 13, Appl	
18	29	29 5	15 1	US-08-487-485A-4	Sequence 4, Appl	
19	29	29 5	17 2	US-08-400-115-26	Sequence 26, Appl	
20	29	29 0	10 2	US-08-637-759B-408	Sequence 408, App	
21	29	29 0	10 3	US-08-871-040-408	Sequence 408, App	
22	29	29 0	10 4	US-09-201-945-408	Sequence 408, App	
23	29	29 0	10 5	PCT-US96-01735-3	Sequence 3, Appl	
24	29	29 0	13 3	US-08-651-136C-102	Sequence 102, App	
25	29	29 0	13 3	US-08-651-136C-104	Sequence 102, App	
26	29	29 0	13 4	US-09-229-911A-102	Sequence 104, App	
27	29	29 0	13 4	US-09-229-911A-104	Sequence 104, App	

ALIGNMENTS

RESULT 1
US-08-983-157B-22
; Sequence 22, Application US/08983157B
; Patent No. 6579848
; GENERAL INFORMATION:
; APPLICANT: HEARING, Vincent J., Jr.
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Peptides and Peptides Thereof
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 127 Peachtree St., N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983-157B
; FILING DATE: 22-Dec-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10695
; FILING DATE: 21 JUN 1996
; APPLICATION NUMBER: 60/ 000,436
; FILING DATE: 23 JUN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 14014.0195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-08-983-157B-22
; Query Match Score 37.0%; DB 4; Length 10;
; Best Local Similarity 66.7%; Pred. No. 15;
; Matches 6; Conservative 1; Mismatches 1;
; Indels 0; Gaps 0;

Qy 8 STNTFCCKP 16
 :|||
 Db 1 ATNDSCCKPP 9

RESULT 2
 US-09-644-600-78
 Sequence 78, Application US/09644600
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Tanimoto, Hirotoshi
 TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
 TITLE OF INVENTION: Overexpressed in Carcinomas
 FILE REFERENCE: D6064CIP/D
 CURRENT APPLICATION NUMBER: US/09/644,600
 CURRENT FILING DATE: 2000-08-23
 PRIORITY NUMBER: 09/421,213
 PRIOR FILING DATE: 1999-10-20
 PRIOR APPLICATION NUMBER: 09/027,337
 PRIOR FILING DATE: 1998-02-20
 NUMBER OF SEQ ID NOS: 98
 SEQ ID NO 78
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Residues 495-503 of the TAGD-15 protein
 US-09-644-600-78

Qy 10 NTFCCKP 15
 :|||
 Db 4 NKFCCKP 9

Query Match 32.0%; Score 32; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Query Match 32.0%; Score 32; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

RESULT 3
 US-09-654-600A-78
 Sequence 78, Application US/09654600A
 GENERAL INFORMATION:
 PATENT NO. 6649741
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Tanimoto, Hirotoshi
 TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
 FILE REFERENCE: D6064CIP/D
 CURRENT APPLICATION NUMBER: US/09/654,600A
 CURRENT FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: 09/421,213
 PRIOR FILING DATE: 1999-10-20
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 OTHER INFORMATION: Residues 495-503 of the TAGD-15 protein
 US-09-654-600A-78

Query Match 32.0%; Score 32; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

RESULT 4
 US-09-053-079A-4
 Sequence 4, Application US/08053079A
 GENERAL INFORMATION:
 PATENT NO. 5606026
 APPLICANT: Rodman
 TITLE OF INVENTION: Natural Human IgM Antibodies
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Darby & Darby
 STREET: 805 Third Ave.
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/053,079A
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Robinson, Joseph, R.
 REGISTRATION NUMBER: 33,448
 REFERENCE/DOCKET NUMBER: 4436/16060USA4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)527-7700
 TELEFAX: (212)753-6237
 TELEX: 236687
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 STRANDEDNESS: Single
 TYPE: amino acid
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Human immunodeficiency virus type 1
 IMMEDIATE SOURCE:
 CLONE: Tat #4
 US-08-053-079A-4

Query Match 32.0%; Score 32; DB 1; Length 12;
 Best Local Similarity 55.6%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 3;

Qy 9 TNTFCKKPPC 17
 :|||
 Db 2 TNFCCKKCC 10

RESULT 5
 US-08-658-589A-228
 Sequence 228, Application US/0868589A
 PATENT NO. 5916872
 GENERAL INFORMATION:
 APPLICANT: Chang, Conway
 APPLICANT: Gu, Leo
 APPLICANT: Chen, Jie
 TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD SPECTRUM ANTIMICROBIAL ACTIVITY
 NUMBER OF SEQUENCES: 222
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York

STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,589A
 FILING DATE: 24-JUL-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEX: 66141

INFORMATION FOR SEQ ID NO: 228:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 NAME/KEY: Peptide
 LOCATION: 1..12
 OTHER INFORMATION: /product= "Cyclic"
 FEATURE: Modified-site
 LOCATION: 12
 OTHER INFORMATION: /product= "Xaa=Cha=cyclohexylalanine"
 US-08-685-589A-228

Query Match Similarity 32.0%; Score 32; DB 2; Length 12;
 Best Local Matches 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 FCKPPC 17
 Db 2 FCKPFC 7

RESULT 6
 US-09-462-118-4
 Sequence 4, Application US/09462118
 Patent No. 6610833
 GENERAL INFORMATION:
 APPLICANT: Riddman, Toby C.
 TITLE OF INVENTION: Monoclonal Human Natural Antibodies
 FILE REFERENCE: 4436/1C074-US1
 CURRENT APPLICATION NUMBER: US/09/462,118
 CURRENT FILING DATE: 1999-12-18
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Human
 US-09-462-118-4

Query Match Similarity 32.0%; Score 32; DB 4; Length 12;
 Best Local Matches 55.6%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 TNTFCKPPC 17
 || : |

Db 2 TNCYCKKCC 10

RESULT 7
 US-08-369-566-1
 Sequence 1, Application US/08369566
 Patent No. 5650151
 GENERAL INFORMATION:
 APPLICANT: Bausher, Michael G
 TITLE OF INVENTION: Citrus Proteins for Use in Field Detection of Citrus Blight Using Immunological Techniques
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: USDA-ARS
 STREET: Room 408, Bldg 005, BARC-W
 CITY: Beltsville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20705

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/369,566
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/792,508
 FILING DATE:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-344-1003
 TELEFAX: 301-344-5060
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-369-566-1

Query Match Similarity 32.0%; Score 32; DB 1; Length 16;
 Best Local Matches 54.5%; Pred. No. 1.4e+2;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GKSTNTPKCPP 16
 || : | | |
 Db 1 GEGTATFYTPP 11

RESULT 8
 US-08-983-157B-21
 Sequence 21, Application US/08983157B
 Patent No. 6579848
 GENERAL INFORMATION:
 APPLICANT: HEARING, Vincent J., Jr.
 TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Protein and Peptides Thereof
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Needle & Rosenberg, P.C.
 STREET: 127 Peachtree St., N.E.
 STATE: GA
 COUNTRY: USA
 ZIP: 30303-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/983,157B
 FILING DATE: 22-Dec-1997
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10695
 FILING DATE: 21 JUN 1996
 APPLICATION NUMBER: 60/ 000,436
 FILING DATE: 23 JUN 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Spratt, Gwendolyn D.
 REGISTRATION NUMBER: 36,016
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 14014.0195
 TELEPHONE: (404) 688-0770
 TELEFAX: (404) 688-9880
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 us-08-983-157B-21

Query Match 31.0%; Score 31; DB 4; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0;
 Gaps 0;

Qy 8 STNTFKPP 16
 Db 1 ATRDSCPP 9

RESULT 9
 US-09-328-501-4
 Sequence 4, Application US/09328501A
 Patent No. 625851

GENERAL INFORMATION:
 APPLICANT: OKINO, No. 62585810mu
 APPLICANT: ITO, Makoto
 TITLE OF INVENTION: Ceramidase Gene
 FILE REFERENCE: 1422-0377P
 CURRENT FILING DATE: 1999-06-09
 EARLIER APPLICATION NUMBER: 10-234769 JAPAN
 EARLIER FILING DATE: 1998-08-20
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 16
 TYPE: PRT
 FEATURE:
 OTHER INFORMATION: any n or Xaa = Unknown
 us-09-328-501-4

Query Match 31.0%; Score 31; DB 3; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0;
 Gaps 0;

Qy 3 SBLGKSTNTF 12
 Db 2 SEIGGSTRSF 11

RESULT 10
 US-09-777-710A-4
 Sequence 4, Application US/09777710A
 Patent No. 6489117
 GENERAL INFORMATION:
 APPLICANT: OKINO, No. 64891170mu et al.

TITLE OF INVENTION: CERAMIDASE GENE
 FILE REFERENCE: 1422-0458P
 CURRENT APPLICATION NUMBER: US/09/777,710A
 CURRENT FILING DATE: 2001-02-07
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 4
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 us-09-777-710A-4

Query Match 31.0%; Score 31; DB 4; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0;
 Gaps 0;

Qy 3 SETGKSTNTF 12
 Db 2 SEIGGSTRSP 11

RESULT 11
 US-08-882-046-9
 Sequence 9, Application US/08882046
 Patent No. 6136952

GENERAL INFORMATION:
 APPLICANT: Lii, Linheng
 APPLICANT: Hood, Leroy
 APPLICANT: Krantz, Tim D.
 APPLICANT: Spinner, Nancy B.
 TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
 TITLE OF INVENTION: Nucleic Acids and Methods of Use
 NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA

ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/882,046
 FILING DATE: 25-JUN-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UW 2637
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 us-08-882-046-9

Query Match 31.0%; Score 31; DB 3; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0;
 Gaps 0;

Qy 6 GKSTNTFCKP 15
 Db 7 GFGCNKFCRP 16

RESULT 12
US-09-252-586-19
Sequence 19, Application US/09252586
Patent No. 6387643

GENERAL INFORMATION:
APPLICANT: Henriksson, Robert L.
APPLICANT: Fairbanks, Michael B.
APPLICANT: Mildner, Ana M.

TITLE OF INVENTION: Human Platelet Heparanase Polypeptides
TITLE OF INVENTION: Polynucleotide Molecules That Encode Them, and Methods For
TITLE OF INVENTION: the Identification of Compounds That Alter Heparanase

TITLE OF INVENTION: Activity

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn
STREET: 301 Henrietta
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,586

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6131.N CN1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-0974
TELEFAX: 616-831-8897

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

US-09-252-586-19

Query Match 31.0%; Score 31; DB 4; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ELGRKSTNTCK 14
Db 7 ELGNEPNNSFLK 17

RESULT 13
US-08-443-965B-9
Sequence 9, Application US/08443965B
Patent No. 5821341

GENERAL INFORMATION:
APPLICANT: McClelland, Alan
APPLICANT: Greve, Jeffrey M.

TITLE OF INVENTION: Soluble Molecule Related to but
TITLE OF INVENTION: Distinct from ICAM-1

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB storage

RESULT 14
US-08-425-989B-9
Sequence 9, Application US/08425989B
Patent No. 5846699

GENERAL INFORMATION:
APPLICANT: McClelland, Alan
APPLICANT: Greve, Jeffrey M.
TITLE OF INVENTION: Soluble Molecule Related to but
TITLE OF INVENTION: Distinct from ICAM-1

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB storage

RESULT 15
US-08-443-965B-9
Sequence 9, Application US/08443965B
Patent No. 5821341

GENERAL INFORMATION:
APPLICANT: McClelland, Alan
APPLICANT: Greve, Jeffrey M.

TITLE OF INVENTION: Soluble Molecule Related to but
TITLE OF INVENTION: Distinct from ICAM-1

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB storage

OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/425, 989B
 FILING DATE: 20-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/156, 653
 FILING DATE: 22-NOV-1993
 APPLICATION NUMBER: 08/005, 204
 FILING DATE: 15-JAN-1993
 APPLICATION NUMBER: 07/449, 356
 FILING DATE: 21-DEC-1989
 APPLICATION NUMBER: 07/449, 356
 FILING DATE: 21-DEC-1989
 APPLICATION NUMBER: 07/445, 951
 FILING DATE: 13-DEC-1989
 APPLICATION NUMBER: 07/301, 192
 FILING DATE: 24-JAN-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbara A. Shimek
 REGISTRATION NUMBER: MTI 209.2C3D1
 REFERENCE/DOCKET NUMBER: MTI 209.2C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 812-2786
 TELEFAX: (203) 812-5492
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acid residues
 TYPE: amino acid residues
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: no
 FRAGMENT TYPE: C-terminal fragment
 FEATURE: modified ICAM fragment
 NAME KEY: modified ICAM fragment
 LOCATION: C-terminus
 OTHER INFORMATION: first 11 amino acid residues correspond to the C-terminus of ICAM; last residue (Cys) added to facilitate coupling
 OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate coupling
 US-08-425-989B-9

Query Match Score 30; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 NTFCRKPPC 17
 Db 7 NTQATPPC 14

RESULT 15
 US-08-443-966B-9
 Sequence 9, Application US/08443966B
 Patent No. 5,859,212
 GENERAL INFORMATION:
 APPLICANT: McClelland, Alan
 APPLICANT: Greve, Jeffrey M.
 TITLE OF INVENTION: Soluble Molecule Related to but Distinct from ICAM-1
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bayer Corporation
 STREET: 400 Morgan Lane
 CITY: West Haven
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06516
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" diskette, 1.44 MB storage
 COMPUTER: IBM ThinkPad 760BD
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect 6.1
 CURRENT APPLICATION DATA:

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 11:00:28 ; Search time 11.6667 Seconds

(without alignments)

74.205 Million cell updates/sec

Perfect score: 55

Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: PIR1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	24	43.6	9	2	C24180		fibrinogen beta ch leucine-tRNA ligas hypothetical TCL3
2	19	34.5	8	2	PC1002		fibronogen beta ch T-cell receptor beta jacinlin beta II ch Y protein - human
3	18	32.7	6	4	I79564		T-cell receptor be fibronopeptide B - fibronopeptide B - fibronopeptide B - T-cell receptor be T-cell receptor be lipopeptide WS1279 calsequitin, fas metallothionein, fas acylase - Kluyvera ferredoxin a2 - Ja transaldolase (B32881) cardioactive pepti T-cell receptor be cardioactive pepti dihydrofolate redu Na+/K+-exchanging galactose oxidase aspartate kinase (calsequestrin, car octameric-binding pr
4	18	32.7	9	2	D24180		
5	18	32.7	9	2	PH0942		
6	17	30.9	6	2	S29637		
7	17	30.9	6	2	I37263		
8	17	30.9	7	2	PH0932		
9	17	30.9	9	2	D28854		
10	17	30.9	9	2	E28854		
11	17	30.9	9	2	F28854		
12	16	29.1	9	2	PH0355		
13	16	29.1	9	2	PH0921		
14	15	27.3	6	2	JU0355		
15	15	27.3	7	2	B39040		
16	15	27.3	8	2	S59622		
17	15	27.3	8	2	S19288		
18	15	27.3	8	2	S69165		
19	15	27.3	9	2	A11497		
20	15	27.3	9	2	A25163		
21	15	27.3	9	2	S27233		
22	15	27.3	9	2	PH0917		
23	15	27.3	9	2	S39167		
24	14	25.5	6	2	B31263		
25	14	25.5	6	2	S29881		
26	14	25.5	7	1	XEINGD		
27	14	25.5	8	2	B47594		
28	14	25.5	9	2	A51230		
29	14	25.5	9	2	B39504		

ALIGNMENTS

RESULT 1
C24180
Fibrinogen beta chain - Japanese macaque (fragment)
N; Contains: fibrinopeptide B
C; Species: Macaca fuscata (Japanese macaque)

C; Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
R; Nakamura, S.; Takenaka, O.; Takahashi, K.

C; Accession: C24180
J. Biochem. 97, 1487-1492, 1985
A; Title: Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and patas monkey (E

uenons, and baboons
A; Reference number: A91990; PMID: 85289140; PMID: 3928610

A; Molecule type: protein
A; Residues: 1-9 <NAK>

C; SuperFamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Query Match 43.6% ; Score 24 ; DB 2 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 2 . 8e+05 ;
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

RESULT 3
 I79564 hypothetical TCL3 protein (mistranslated) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
 C;Accession: I79564
 R;Zutter, M.; Rockert, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;
 PROC.Natl.Acad.Sci.U.S.A. 87, 3161-3165, 1990
 A;Title: The t(10;14) (q21;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del
 A;Reference number: 159162; PMID:90222189; PMID:2326274
 A;Accession: I79564
 A;Status: translation not shown; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <ZUT>
 A;Cross-references: GB:M33602; NID:9339907; PID:9807656
 C;Comment: This is the hypothetical translation of a sequence translated in an incorrect
 Query Match 32.7%; Score 18; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CC 2
 Db 3 CC 4

Qy 1 CC 2
 Db 1 CC 2

RESULT 4
 D4180 fibrinogen beta chain - red guenon (fragment)
 N;Contains: fibrinopeptide B
 C;Species: Erythrocebus patas (red guenon, hussar)
 C;Accession: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 97, 1487-1492, 1985
 A;Title: Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and patas monkey (*E. unicolor*, and baboons.)
 A;Reference number: A91990; PMID:85289140; PMID:3928610
 A;Accession: D24180
 A;Molecule type: protein
 A;Residues: 1-9 <NAK>
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfuf
 Query Match 32.7%; Score 18; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 NEESL 7
 Db 1 NEEVL 5

Qy 1 NEEV 2
 Db 1 NEEV 2

RESULT 5
 PH0942 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0942
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A;Reference number: PH0942; PMID:92078857; PMID:1836012
 A;Accession: PH0942
 A;Molecule type: mRNA
 A;Residues: 1-9 <GOL>
 A;Experimental source: complete Freund's adjuvant-immunized lymph node
 A;Note: the authors transcribed the codon TGC for residue 2 as Ala
 C;Keywords: T-cell receptor

Query Match 32.7%; Score 18; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 S29637 jacalin beta-II chain - Artocarpus champeden (fragment)
 C;Species: Artocarpus champeden
 C;Date: 19-Mar-1998 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
 C;Accession: S29637
 R;Ngoc, L.D.; Brillard, M.; Hoebeke, J.
 Biochim. Biophys. Acta 1156, 219-222, 1993
 A;Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
 A;Reference number: S29635; PMID:33152201; PMID:8427879
 A;Experimental source: seed
 A;Molecule type: protein
 A;Residues: 1-6 <NGO>
 A;Keywords: heterotetramer; lectin; seed; storage protein

Query Match 30.9%; Score 17; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NEES 6
 Db 1 NEOS 4

RESULT 7
 I37263 Y protein - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I37263
 R;Waerber, G.; Habener, J.F.
 Endocrinology 131, 2010-2015, 1992
 A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an altern
 A;Reference number: I37263; PMID:13901691; PMID:1396344
 A;Accession: I37263
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: EMBL:X68994; NID:9396171; PID:9579816
 C;Genetics:
 A;Gene: CREB

Query Match 30.9%; Score 17; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLIC 9
 Db 1 SLFC 4

RESULT 8
 PH0932 T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0932
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A;Reference number: PH0932
 A;Accession: PH0932

Query Match 30.9%; Score 17; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Molecule type:	mRNA
Residues:	1-7 <GO!>
Experimental source:	complete Freund's adjuvant-immunized lymph node
Keywords:	T-cell receptor
Query Match	30.9%; Score 17; DB 2; Length 7;
Best Local Similarity	42.9%; Pred. No. 2.8e-05;
Matches	3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Y	1 CCNESSL 7 : 1 CASPERL 7

RESULT 9
D28854

librinopeptide B - olive baboon
Species: Papio anubis, Papio hamadryas anubis (olive baboon)
Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
Accession: D28854
Nakamura, S.; Takenaka, O.; Takahashi, K.
Biochem. 94, 1973-1978, 1983
Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada).
Reference number: A91973; MUID:84161822; PMID:6423621
Accession: D28854
Molecule type: protein
Residues: 1-9 <NAK>
Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match	Score	Length	DB	Pred.	No.	Gaps
Best Local Similarity	30.9%	17	2			0;
Matches	60.0%			$2.8e+05$		
3	Conservative	1;	Mismatches	1;	Indels	0;
3	NEBSI	1	1	1	1	1

SULT 10
8854
brinopeptide B - hamadryas baboon
Species: Papio hamadryas (hamadryas baboon)
Accession: E28854
Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
Accession: E28854
Nakamura, S.; Takenaka, O.; Takahashi, K.
Blochem, 94, 1973-1978, 1983
Title: Fibrinopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*, and *Theropithecus gelada*)
Reference number: A91973; MOLD:8116182; PMID:6123621
Molecule type: protein
Accession: E28854
Residue: 1-9 <NAK>
Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
Query Match 30.0%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Caps 0;
3 NEESL 7
| : | |
1 NQEGL 5

SULT 11
3854
Prinopeptide B - gelada baboon
Species: Theropithecus gelada (gelada baboon)
Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
Accession: F28854
Fukamura, S.; Takenaka, O.; Takahashi, K.
Biochem. 94, 1973-1978, 1983
Title: Fibropitopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada).
Reference number: A91973; MUID:84161822; PMID:6423621
Accession: F28854

A: Molecule type: protein
 A: Residues: 1-9 <NAK>
 C: Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

	Query	Match	Score	DB	Length
Best Local Similarity	3	30.9%	17	2	9
Matches	3	60.0%	Pred. No.	2.8e-05	
Conservative	1	Mismatches	1	Indels	0
				Gaps	0

RESULT 12
 PH0935
 T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0935
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991.
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 A;Reference number: PH0891; PMID:92078857; PMID:1836012
 A;Accession: PH0935
 A;Molecule type: mRNA
 A;Residues: 1-9 <GO>
 A;Experimental source: complete Freund's adjuvant-immunized lymph node
 C;Keywords: T-cell receptor

Query	Match	Score	Length	%
Best	16	DB 2;	9	
Local	32.3%	Pred.	NO.	
Similarity	2;	Conservative	2;	
Matches	2;	Mismatches	2;	
		Indels	0;	Gaps
			0;	0;

CONTINUE 6

RESULT 1.3

PH0921 T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C.Species: Rattus norvegicus (Norway rat)

C.Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C.Accession: PH0921

D.P.: Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.

J.J. Exp. Med.: 174, 1467-1476, 1991

A.Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A.Reference number: PH0891; PMID:1836012

A.Accession: PH0921

A.Molecule type: mRNA

A.Residues: 1-9 <GOL>

A.Experimental source: concanavalin A-activated lymphoblast

C.Keywords: T-cell receptor

Query	Match	Score	DB	Length	9;	
Best	Local Similarity	29.1%	2;			
Matches	2;	33.3%;	Pred.	No.	2.8e+05;	
	Conservative	2;	Mismatches	2;	Indels	
				0;	Gaps	0;

1 CCNEES 6

RESULT 14
 JU0355 ipopeptide WS1279 [validated] - *Streptomyces willmorei*
 Species: *Streptomyces willmorei*
 Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 Accession: JU0355
 Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.,
 them. Pharm Bull. 39, 607-611, 1991
 Title: Structure and synthesis of an immunoactive lipopeptide. WS1279 of microbial or

A;Accession: JU0355
 A;Molecule type: protein
 A;Residues: 1-6 <TSU>
 A;Note: the structure was confirmed by synthesis
 C;Keywords: blocked amino end; lipoprotein
 C;Species: Oryctolagus cuniculus (Cys) (covalent) #status experimental
 F;1/Binding site: sn-2,3-diacylglycerol (Cys) #status experimental
 F;1/Modified site: fatty acylated amino end (Cys) #status experimental
 Qy 2 CN 3
 Db 1 CN 2
 |||

RESULT 15
 B39040 calsequestrin, fast skeletal muscle - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
 C;Accession: B39040
 R.Cala, S.E.; Jones, L.R.
 J.Biol.Chem. 266, 391-398, 1991
 Article: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
 A;Reference number: A39040; MUID:91093153; PMID:1985907
 A;Accession: B39040
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <CAL>
 C;Keywords: phosphoprotein; skeletal muscle

Query Match 27.3% ; Score 15; DB 2; Length 7;
 Best Local Similarity 60.0% ; Pred. No. 2.8e+05;
 Matches 3 ; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 NEESL 7
 Db 2 DEEDL 6
 |||

Search completed: September 5, 2004, 11:06:22
 Job time : 12.6667 secs

DE PIR; D28854; D28854;	DR InterPro; IPR002101; Fibrinogen C.
GN ERYTHROCEBUS PATAS (Red guenon) (Hussar).	DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	KW Blood coagulation; Plasma.
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
OC Cercopithecinae; Erythrocebus.	FT NON-TER 9 9
OX NCBI_TAXID=9538;	SQ SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;
RN [1]	
RP SEQUENCE-85289140; PubMed=3928610;	Query Match Score 30.9%; Pred. No. 1.4e+05; Best Local Similarity 60.0%; Matches 3; Conservative 1; Indels 0; Gaps 0;
RX MEDLINE=85289140;	PRT; 9 AA.
RA Nakamura S.; Takenaka O.; Takahashi K.; RT "Fibrinopeptides A and B of Japanese monkey (<i>Macaca fuscata</i>) and patas monkey (<i>Bryttocebus patas</i>): their amino acid sequences, restricted mutations, and a molecular phylogeny for macaques, guenons, and baboons.";	AC P19343; (Rel. 16, Created)
RT J. Biochem. 97:1487-1492 (1985).	DT 01-NOV-1990 (Rel. 16, Last sequence update)
RT J. Biochem. 97:1487-1492 (1985).	DT 10-OCT-2003 (Rel. 42, Last annotation update)
RL J. Biochem. 97:1487-1492 (1985).	DE Fibrinogen beta chain [Contains: Fibropeptide B] (Fragment).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.	GN PGB
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	OS Papio hamadryas (<i>Hamadryas baboon</i>);
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; NCBI_TAXID=9557;
CC DR D24180; D24180.	RN [1]
DR InterPro; IPR002181; Fibrinogen C.	PP SEQUENCE; MEDLINE=64161822; PubMed=64233621;
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.	RX Nakamura S.; Takenaka O.; Takahashi K.; i
KW Blood coagulation; Plasma.	RA Papio hamadryas (<i>Papio anubis</i> , <i>Papio hamadryas</i> ,
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.	RT "Fibrinopeptides A and B of baboons" their amino acid sequences and
FT NON-TER 9 9	RT and <i>Theropithecus gelada</i> : their amino acid sequences and
SQ SEQUENCE 9 AA; 1020 MW; 69FB7879C732CB1B CRC64;	RT evolutionary rates and a molecular phylogeny for the baboons.";
RN [1]	RL J. Biochem. 94:1973-1978 (1983).
Query Match Score 32.7%; Pred. No. 1.4e+05; Best Local Similarity 80.0%; Matches 4; Conservative 0; Indels 0; Gaps 0;	CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.
PRT; 9 AA.	CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
AC P19344; (Rel. 16, Created)	CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
DT 01-NOV-1990 (Rel. 16, Last sequence update)	DR PIR; E28854; E28854.
DT 10-OCT-2003 (Rel. 42, Last annotation update)	DR InterPro; IPR002181; Fibrinogen C.
DB Fibrinogen beta chain [Contains: Fibropeptide B] (Fragment).	DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
GN PGB.	KW Blood coagulation; Plasma.
OS Papio anubis (Olive baboon).	FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT NON-TER 9 9
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	SQ SEQUENCE 9 AA; 1057 MW; DDFE7119C7287B06 CRC64;
NCBI_TAXID=9555;	Query Match Score 30.9%; Pred. No. 1.4e+05; Best Local Similarity 60.0%; Matches 3; Conservative 1; Indels 0; Gaps 0;
RN [1]	PRT; 9 AA.
RP SEQUENCE-84161822; PubMed=64233621;	AC P19342; (Rel. 16, Created)
RX MEDLINE=84161822;	DT 01-NOV-1990 (Rel. 16, Last sequence update)
RA Nakamura S.; Takenaka O.; Takahashi K.; RT "Fibrinopeptides A and B of baboons (<i>Papio anubis</i> , <i>Papio hamadryas</i> , and <i>Theropithecus gelada</i>): their amino acid sequences and	DT 10-OCT-2003 (Rel. 42, Last annotation update)
RT evolution rates and a molecular phylogeny for the baboons.";	DE Fibrinogen beta chain [Contains: Fibropeptide B] (Fragment).
RL J. Biochem. 94:1973-1978 (1983).	CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
CC -!- PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.	CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PRT; 9 AA.	CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
AC P19342; (Rel. 16, Created)	CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.
DT 01-NOV-1990 (Rel. 16, Last sequence update)	CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
DT 10-OCT-2003 (Rel. 42, Last annotation update)	CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
DB 1 NQBGL 5	CC -!- PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
RN [1]	Query Match Score 30.9%; Pred. No. 1.4e+05; Best Local Similarity 60.0%; Matches 3; Conservative 1; Indels 0; Gaps 0;
PRT; 9 AA.	PRT; 9 AA.

GN Theropithecus gelada (Gelada baboon).
 OS Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Theropithecus.
 OX NCBI_TaxID=9565;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=84161822; PubMed=6423621;
 RA Nakamura S., Takekawa O., Takahashi K.;
 RT "Fibrinopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*,
 and *Theropithecus gelada*): their amino acid sequences and
 evolutionary rates and a molecular phylogeny for the baboons.";
 RT J. Biochem. 94:1973-1978 (1983).
 RL Polymerization has a double function: yielding monomers that
 polymerize into fibrin and acting as a cofactor in platelet
 aggregation.

CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 which cleaves fibrinopeptides A and B from alpha and beta chains,
 and thus exposes the N-terminal polymerization sites responsible
 for the formation of the soft clot.

CC PIR: F28854; F28854.

DR InterPro; IPR002181; Fibrinogen C.

DR PROSITE; PS00514; FIBRIN AG_C_DOMAIN; PARTIAL.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 9 FIBRINOPEPTIDE B.

FT NON_TER 9 9 DDFE7879C7287B06 CRC64;

SEQUENCE 9 AA; 977 MW;

Query Match 30 9%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
 :|:
 Db 1 NOEGL 5

RESULT 6
 ID ULAK_MOUSE STANDARD PRT; 9 AA.

AC P99071; (Rel. 37, Created)

DT 15-DESC-1998 (Rel. 37, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
 (Fragment).

OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

NCBI_TaxID=10050;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted [AUG-1998] to Swiss-Prot.

CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.0. its MW is: 12.5 kDa.

DR SWISS-2DPAGE; P99031; MOUSE.

DR NON_TER 9 9 DR

FT SEQUENCE 9 AA; 1106 MW; ELE842C3240B145A CRC64;

SQ Score 16; DB 1; Length 9;

Query Match 29.1%; Score 16; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NEESL 8
 :|:
 Db 3 NERKVI 8

RESULT 7

CCAP_CARMA STANDARD PRT; 9 AA.

ID CCAP_CARMA P38556;

AC DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DB Cardioactive Peptide (CCAP).

OS Carcinus maenas (Common shore crab) (Green crab),

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),

OS Tenebrio molitor (Yellow mealworm), and

OS Spodoptera eridania (Southern armyworm).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Bivalacostraca; Bucardiida; Decapoda; Pleocyemata; Portunidae; Carcinus.

NCBI_TaxID=6759, 7130, 7067, 37547;

RN [1]

RP SEQUENCE.

RC SPECIES=C. maenas; TISSUE=Pericardial organs;

RC STANGIER J., HILBICH C., BEYREUTHER K., KELLER R.;

RA "Unusual cardioactive peptide (CCAP) from pericardial organs of the

RT shore crab *Carcinus maenas*";

RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).

RN [2]

RP SEQUENCE.

RC SPECIES=M. sexta; TISSUE=Head;

RC MEDLINE=3305043; PubMed=1426284;

RX RX

RA Cheung C.C., Lai P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;

RT "Primary structure of a cardioactive neuropeptide from the tobacco

RT RT shore crab *Carcinus maenas*";

RL FEBS Lett. 313:165-168 (1992).

RN [3]

RP SEQUENCE.

RC SPECIES=T. molitor, and S. eridania; TISSUE=Head;

RC MEDLINE=9417632; PubMed=8129851;

RX RX

RA Schooley D.A.;

RA RT "Isolation and identification of a cardioactive peptide from *Tenebrio*

RT *molitor* and *Spodoptera eridania*";

CC CC

CC -!- FUNCTION: The effect of CCAP is both ino-

CC -!- SUBCELLULAR LOCATION: Secreted.

CC CC

CC -!- TISSUE SPECIFICITY: Stored in pericardial organs and released

CC CC into the hemolymph.

DR DR

PIR: A26363; A26363.

DR DR

PIR: S27233; S27233.

KW KW Neuropeptide; Amidation.

FT FT DISULFID

3 3 AMIDATION.

FT FT MOD RES

SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

RN SQ 27.3%; Score 15; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

TAL3_PICJA STANDARD PRT; 9 AA.

ID TAL3_PICJA P17441;

AC AC

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE DE Transaldolase III (EC 2.2.1.2) (Fragment).

OS Pichia jadinii (Yeast) (Candida utilis).

OC Saccharomyces; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Pichia.

OX NCBI_TAXID=4903;
 RN [1] _
 RP SEQUENCE.
 RX MEDLINE=75145197; PubMed=1092268;
 RA Tsolas O., Sun S.C.;
 RT "Isolation of a peptide containing a histidinyl-cysteinyl sequence from the active center of transaldolase";
 RL Arch. Biochem. Biophys. 167:525-533 (1975).
 CC -!- FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway.
 CC -!- CATALYTIC ACTIVITY: Seddheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
 DR PIR; Al1497; Al1497.
 DR InterPro; IPR001585; Transaldolase.
 DR PROSITE; PS00958; TRANSDOLASE_2; PARTIAL.
 DR PROSITE; PS01054; TRANSDOLASE_1; PARTIAL.
 KW Transferase; Pentose shunt.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1033 MW; 325431AA4EB18058 CRC64;
 Query Match Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 CN 3
 Db 5 CN 6
 RESULT 9
 ID IGAO_DACDB STANDARD; PRT; 7 AA.
 AC P06294;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Galactose oxidase inhibitor.
 OS Dactyloctenium dendroides (Cladobotryum dendroides).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
 OX NCBI_TAXID=5132;
 RN SEQUENCE.
 RA Avigad G., Markus Z.;
 RT "Identification of a peptide inhibitor of galactose oxidase from Dactyloctenium dendroides.";
 RL Fed. Proc. 31:447-447(1972).
 CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the galactose oxidase apoenzyme. It may inactivate the enzyme by binding to its prosthetic copper group.
 DR PIR; A01341; XEYGD.
 KW Copper; Metalloenzyme inhibitor.
 SQ SEQUENCE 7 AA; 706 MW; 75BB01AA456D87DB0 CRC64;
 Query Match Score 14; DB 1; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 NBES 6
 Db 4 NBES 7
 RESULT 10
 ID TRM3_ECOLI STANDARD; PRT; 5 AA.
 AC P13973;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tram protein (Fragment).
 RN TRAM;
 RN SEQUENCE FROM N.A. PMID=2836369;
 RX MEDLINE=88227859; PubMed=2836369;
 RA Inamoto S., Yoshioka Y., Ohtsubo E.;
 RT "Identification and characterization of the products from the traJ and traY genes of plasmid R100.";
 RT J. Bacteriol. 170:2749-2757(1988).
 CC -!- FUNCTION: TRANSFER GENE PROTEIN IS INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the traM family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See: http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
 CC DR EMBL; M20941; -; NOT_ANNOTATED_CDS.
 CC DR PIR; A32014; A32014; -; NOT_ANNOTATED_CDS.
 KW Conjugation; Plasmid; DNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;
 Query Match Score 13; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 NEE 5
 Db 2 NDE 4
 RESULT 11
 ID PLP_BRANA STANDARD; PRT;
 AC P81707;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DB Plastidial lipid-associated protein (Fragment).
 OS Brassica napus (Rapeseed).
 CC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicots; rosids;
 OC eurotids II; Brassicales; Brassicaceae; Brassicaceae; Brassicaceae.
 OX NCBI_TAXID=3708;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV_TOPAZ; TISSUE=Tapetum;
 RX MEDLINE=9349136; PubMed=10420651;
 RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
 RA Murphy D.J.;
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of Brassica napus.";
 RL Plantae 208:588-598(1999).
 CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-specific plastidial lipid organelle.
 CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452GAA042 CRC64;

Qy	3 NEE 5	SQ	SEQUENCE	7 AA;	842 MW;	6AA72B1DDDB1B1180 CRC64;
Db	5 NDE 7	Query Match	Score 21.8%; Best Local Similarity 50.0%; Matches 2;	DB 1; Pred. No. 1.4e+05; Mismatches 2;	Length 7; Indels 0;	Gaps 0;
		Qy	3 NEES 6			
		Db	: :			
			1 HEEA 4			
RESULT 12						
SAMP_MUSCA	STANDARD;	PRT;	9 AA.			
AC P19095;						
DT 01-NOV-1990 (Rel. 16, Created)						
DT 01-NOV-1990 (Rel. 16, Last sequence update)						
DT 28-FEB-2003 (Rel. 41, Last annotation update)						
DE Serum amyloid P-component (SAP) (Fragment).						
MS Musculus carnis (Smooth dogfish)						
OS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;						
OC Blasmodibranchii; Galeomorphii; Galleoidea; Carcharhiniformes; Triakidae;						
OC Muscidae.						
OX NCBI_TaxID=7812;						
RN [1]						
RP SEQUENCE;						
RX MEDLINE=83160932; PubMed=6403520;						
RA Robey F.A.; Tanaka T.; Liu T.-Y.;						
RT "Isolation and characterization of two major serum proteins from the dogfish, <i>Mustelus canis</i> , c-reactive protein and amyloid P component".						
RT [1]						
RT DOMAIN 1 >9 PENTAXIN						
RT PIR: B20569; B20569; Pentaxin.						
DR InterPro; IPR001759; PENTAXIN; PARTIAL.						
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.						
FT DOMAIN 1 >9 PENTAXIN						
FT NON_TER 9						
SQ SEQUENCE 9 AA;	965 MW;	D05BS735B3386769 CRC44;				
Query Match	Score 23.6%; Best Local Similarity 75.0%; Matches 3;	DB 1; Pred. No. 1.4e+05; Conservative 1;	Length 9; Indels 0;		Score 13; Pred. No. 1.4e+05; Conservative 1;	DB 1; Indels 0;
Qy	5 ESLI 8	OY	3 NEES 6			
Db	5 KSLI 8	Db	:			
			1 DQES 4			
RESULT 13						
UF03_MOUSE	STANDARD;	PRT;	7 AA.			
AC P38641;						
DT 01-OCT-1994 (Rel. 30, Created)						
DT 01-OCT-1994 (Rel. 30, Last sequence update)						
DT 15-MAR-2004 (Rel. 43, Last annotation update)						
DB Unknown protein from 2D-page of fibroblasts (P36) (Fragment).						
OS Mus musculus (Mouse).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX NCBI_TaxID=10090;						
RN [1]						
RP SEQUENCE.						
RC TISSUE=Fibroblast;						
RX MEDLINE=95009907; PubMed=7523108;						
RA Merrick B.A.; Patterson R.M.; Wichter L.L.; He C.; Selkirk J.K.;						
RT "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis";						
RT Electrophoresis 15:735-745(1994).						
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is 5.1, its MW is 36 kDa.						
FT NON_TER 7						

Query Match	Score 21.8%; Best Local Similarity 50.0%; Matches 2;	DB 1; Pred. No. 1.4e+05; Conservative 0;	Length 7; Indels 0;	Gaps 0;		
Qy	3 NEES 6	OY	3 NEES 6			
Db	: :	Db	1 DQES 4			
RESULT 14						
UPA1_HUMAN	STANDARD;	PRT;	8 AA.			
AC P30087;						
DT 01-APR-1993 (Rel. 25, Created)						
DT 01-APR-1993 (Rel. 25, Last sequence update)						
DT 15-MAR-2004 (Rel. 43, Last annotation update)						
DB Unknown protein from 2D-page of plasma (Spot 2) (Fragment).						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX NCBI_TaxID=9606;						
RN [1]						
RP SEQUENCE.						
RC TISSUE=Plasma;						
RX MEDLINE=9302937; PubMed=1459097;						
RA Hughes G.J.; Prutiger S.; Paquet N.; Ravier F.; Pasquali C., Sanchez J.-C., James R., Tissot J.-D., Belykqvist B., Hochstrasser D.F.;						
RA "Plasma protein map: an update by microsequencing.";						
RA "Electrophoresis 13:707-714(1992)."						
RL "Miscellaneous: On the 2D-gel, the determined pI of this unknown protein is 4.9, its MW is: 65 kDa.						
CC -!- MISCELLANEOUS: On the 2D-gel, the determined pI of this unknown protein is 4.9, its MW is: 65 kDa.						
CC SWISS-2DPAGE; P30087; HUMAN.						
DR NON_TER 1						
FT UNSURE 8						
SQ SEQUENCE 8 AA;	944 MW;	C01772C455BB06DA CRC64;				
Query Match	Score 21.8%; Best Local Similarity 50.0%; Matches 2;	DB 1; Pred. No. 1.4e+05; Conservative 0;	Length 8; Indels 0;	Gaps 0;		
Qy	3 NEES 6	OY	3 NEES 6			
Db	:	Db	1 DQES 4			
RESULT 15						
SAP_STOVA	STANDARD;	PRT;	9 AA.			
ID SAP_STOVA						
AC P24547;						
DT 01-MAR-1992 (Rel. 21, Created)						
DT 01-MAR-1992 (Rel. 21, Last sequence update)						
DT 10-OCT-2003 (Rel. 42, Last annotation update)						
DE Stom-p-activating Peptide (SAP).						
OS Stomopneutes variolaris (Sea urchin).						
OC Echinoida; Metazoa; Eutherozoa; Echinozoa;						
OC Echinoidae; Euechinoidea; Diadematacea; Phymosomatoidae; Stomechinidae;						
OC Stomopneustes.						
OX NCBI_TaxID=7663;						
RN [1]						
RP SEQUENCE, AND DISULFIDE BOND.						
RC TISSUE=Egg jelly;						
RX MEDLINE=2097763; PubMed=1756858;						
RA Yoshimoto K.-I.; Takeo T.; Shimomishi Y., Suzuki N.;						
RT "Determination of the amino acid sequence of an intramolecular disulfide linkage-containing sperm-activating peptide by tandem mass spectrometry";						
RT FEBS Lett. 294:179-182(1991)						
CC -!- FUNCTION: Cause stimulation of sperm respiration and motility through intracellular alkalinization, transient elevations of						

CC cAMP, cGMP and calcium levels in sperm cells, and transient activation and subsequent inactivation of the membrane form of CC S-nitrolylase cyclase.
CC
FT DISULFID 3 8
SEQUENCE 9 AA; 1010 MW; C469B3387B076BB9 CRC64;
Query Match 21.8%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Prod. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CNE 4
|
Db 3 CPE 5

Search completed: September 5, 2004, 11:04:00
Job time : 7 secs

Copyright (C) 1993 - 2004 Compugen Inc.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:59:47 ; Search time 31.6667 Seconds
(without alignments)

89.674 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNEBSLIC 9

Scoring table: BL050M62

Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Maximum Match 0%

Listing First 45 summaries

Database : SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate

DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	OS	Mus musculus (Mouse);		
DE	Phosoglucose isomerase (Fragment).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS	Dioscorea tokoro.	OC	Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae;		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC	Mus.		
OC	Spermatophytia; Magnoliophyta; Liliopsida; Dioccoreales; Dioscoreaceae;	OC			
ON	Dioscorea.	NCBI_TAXID=64475;			
RN	[1]	NCBI_TAXID=64475;			
RP	SEQUENCE FROM N.A.				
RC	STRAIN-DT17-1;				
XX	PMID=2079211; PubMed=10821191;				
RA	Terauchi R., Kahl G.;				
RT	"Rapid isolation of promoter sequences by TAI-PCR: the 5'-flanking				
RT	regions of Pal and PgI genes from yams (Dioscorea).";				
RL	Mol. Gen. 263:554-560(2000).				
DR	EMBL; AB016716; BAA3235.1; -				
DR	GO; GO:0016853; P:isomerase activity; IEA.				
RW	Isomerase.				
FT	NON_TER				
SEQUENCE	8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;				
Qy	6 SLIC 9 :				
Db	5 TLIC 8				
<hr/>					
RESULT 3					
ID	Q9FSZ2	PRELIMINARY;	PRT;	9 AA.	
AC	Q9FSZ2;				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DB	Hypothetical protein (Fragment).				
OS	Cicer arietinum (Chickpea) (Garbanzo).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophytia; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid I; Fabales; Fabaceae; Papilioideae; Ciceraceae; Cicer.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-N.A.				
RA	Dopico B., Jimenez T., Labrador E.;				
RT	"cDNA clones expressed in etiolated Cicer arietinum epicotyls.";				
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AU299069; CAC10216.1; -				
KW	Hypothetical protein.				
FT	NON_TER				
SEQUENCE	9 AA; 990 MW; 9441BDDAA7272EBE CRC64;				
Qy	32.7%; Score 18; DB 10; Length 9;				
Db	Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;				
<hr/>					
RESULT 4					
ID	Q8CG13	PRELIMINARY;	PRT;	9 AA.	
AC	Q8CG13;				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 24, Last annotation update)				
DE	Glutamate receptor ionotropic N-methyl D-aspartate-like 1A (Fragment).				
GN	GRIN1A.				
<hr/>					
RESULT 5					
ID	Q9E1U7	PRELIMINARY;	PRT;	9 AA.	
AC	Q9E1U7;				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-DBC-2001 (TREMBLrel. 19, Last annotation update)				
DE	X-protein (Fragment).				
GN	X.				
OS	Hepatitis B virus.				
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.				
OX					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-N.A.				
RA	Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;				
RT	"Sequence variation of Hepatitis B virus Promoter regions in persistently infected patients.";				
RT	Permanently infected Patients.";				
RL	Arch. Virol. 146:279-292(2001).				
DR	EMBL; AF216522; AAC29993.1; -				
FT	NON_TER				
SEQUENCE	9 AA; 994 MW; CD0FD8BEA2D4DDDD CRC64;				
Qy	32.7%; Score 18; DB 12; Length 9;				
Db	Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;				
<hr/>					
RESULT 6					
ID	QB6SF0	PRELIMINARY;	PRT;	9 AA.	
AC	QB6SF0;				
DT	01-JUN-2003 (TREMBLrel. 24, Created)				
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Peroxisome proliferator-activated receptor alpha (Fragment).				
GN	PPRA.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

CS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11660;
 RN [1] _

SEQUENCE FROM N.A.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RT "dtrPase minus CAEV is attenuated for pathogenesis and accumulates G
 to A substitutions.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81439; AAB60832.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;

RESULT 13
 ID 012098 PRELIMINARY; PRT; 9 AA.
 AC 012098
 RA 01-JUL-1997 (TREMBLrel. 04, Created)
 RT "dtrPase minus CAEV is attenuated for pathogenesis and accumulates G
 to A substitutions.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR U81440; AAB60835.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;

Query Match 27.3%; Score 15; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CN 3
 DB 6 CN 7

RESULT 14
 ID 012104 PRELIMINARY; PRT; 9 AA.
 AC 012104
 RA 01-JUL-1997 (TREMBLrel. 04, Created)
 RT "dtrPase minus CAEV is attenuated for pathogenesis and accumulates G
 to A substitutions.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR U81440; AAB60840.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;

Query Match 27.3%; Score 15; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CN 3
 DB 6 CN 7

RESULT 15
 ID 012104 PRELIMINARY; PRT; 9 AA.
 AC 012104
 RA 01-JUL-1997 (TREMBLrel. 04, Created)
 RT "dtrPase minus CAEV is attenuated for pathogenesis and accumulates G
 to A substitutions.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR U81443; AAB60843.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;

Query Match 27.3%; Score 15; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CN 3
 DB 6 CN 7

RESULT 16
 ID 012102 PRELIMINARY; PRT; 9 AA.
 AC 012102
 RA 01-JUL-1997 (TREMBLrel. 04, Created)
 RT "dtrPase minus CAEV is attenuated for pathogenesis and accumulates G
 to A substitutions.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR U81442; AAB60838.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;

Query Match 27.3%; Score 15; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 15
Q8MJJ7; PRELIMINARY; PRT; 9 AA.
ID Q8MJJ7;
AC (TRMBLrel. 22, Created)
DT 01-OCT-2002 (TRMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus (Brown lemur).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemuridae; Eulemur.
OC NCBI_TaxID:13515;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Stumpf R., Desalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
zone at Andringitra, Madagascar."
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF258049; AAM43870.1; -
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;
Query Match Similarity 25.5%; Score 14; DB 6; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+06; Gaps 0;
Matches 2; Conservative 2; Mismatches 1; Indels 0;
Oy 4 EBSLI 8
Db 2 EBGIL 6

```

Search completed: September 5, 2004, 11:05:41
 Job time : 32.6667 secs

This Page Blank (uspto)

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	AAU04528	Aau04528 VEGF base
2	50	90.9	9	AAU04552	Aau04552 VEGF base
3	49	89.1	9	AAU04553	Aau04553 VEGF base
4	46	83.6	8	AAU04525	Aau04525 VEGF base
5	43	78.2	8	AAU04539	Aau04539 VEGF base
6	42	76.4	8	AAU04541	Aau04541 VEGF base
7	41	74.5	8	AAU04538	Aau04538 VEGF base
8	39	70.9	8	AAU04540	Aau04540 VEGF base
9	35	63.6	8	AAU08451	Aau08451 Peptide A
10	33	60.0	8	AAU08460	Aau08460 Peptide C
11	33	60.0	9	ABR29819	Abr29819 Human can
12	33	60.0	9	ABR28797	Abr28797 Human can
13	33	60.0	9	ABR29456	Abr29456 Human can
14	33	60.0	9	ABR28814	Abr28814 Human can
15	33	60.0	9	ABR29789	Abr29789 Human can
16	33	60.0	9	ABR28619	Abr28619 Human can
17	33	60.0	9	ABR29608	Abr29608 Human can
18	33	60.0	9	ABR29220	Abr29220 Human can
19	33	60.0	9	ABR29572	Abr29572 Human can
20	33	60.0	9	ABR29383	Abr29383 Human can
21	31	56.4	6	ABR29379	Abr29379 Partial P
22	30	54.5	8	AAV24954	Aar24954 Conformat
23	30	54.5	8	AAV54526	Aav54526 Human CD4
24	29	52.7	9	ABR28842	Abr28842 Human can
25	28	50.9	9	AAW09329	Aaw09329 FIV princ

XX The sequence represents a dimeric bicyclic peptide of the invention, CC whose 3-dimensional structure is modelled on the expose loop of human CC VEGF (vascular endothelial growth factor). The invention relates to a CC method of producing a monomeric monocyclic peptide by a measuring beta- CC beta carbon separation distances on opposite antiparallel strands of a CC peptide loop fragment from an exposed loop of a growth factor protein and CC cyclising the peptide by oxidising the cysteine residues. The monocyclic CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic CC peptides) and a cyclic peptide with at least one amino acid deleted prior CC to cyclisation are used to interfere with angiogenesis. CC neovascularisation or lymphangiogenesis in a mammal with a condition CC characterised by angiogenesis, neovascularisation or lymphangiogenesis. CC The condition is diabetic retinopathy, psoriasis, arthropathy, CC haemangioma, vascularised malignant or benign tumour, post-recovery CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold CC trauma, substance-induced neovascularisation of the liver, excessive CC hormone-related angiogenic dysfunction, diabetes induced neovascular CC sequelae, hypertension induced neovascular sequelae, or chronic liver CC infection. The peptides are also used to modulate vascular permeability CC in a mammal (the mammal has a condition characterised by fluid CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, CC or brain). The peptides are used to image blood vessels and lymphatic CC vasculature. The monomeric and bicyclic peptides are used to interfere CC with at least one biological activity induced by VEGF, VEGF-C or -D and CC also used in combination with an anti-inflammatory agent, to treat a CC chronic inflammation, especially rheumatoid arthritis, psoriasis and CC diabetic retinopathy

SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNBEISLIC 9
| ||| | | | | |
Db 1 CCNBEISLIC 9

RESULT 2
AAU04552
ID AAU04552 standard; peptide; 9 AA.
AC
XX
AC
XX
DT 26-SEP-2001 (first entry)
DE VEGF based bicyclic dimeric peptide #9.

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.

XX Key Location/Qualifiers
FR Disulfide-bond 1
/note= "A disulfide bond forms between residue 1 and residue 17 of the sequence appearing as AAU04527, forming a dimeric peptide"

FR Disulfide-bond 2..9
/note= "This bond cyclises the peptide"
XX WO200152875-A1.
PN 18-JAN-2001; 2001WO-US001533.
XX PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.

XX (LUDWIG INSTITUTION CANCER RES.
PA XX Achen MG, Hughes RA, Stackler S, Cendron A;
PI XX DR; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment PT from an exposed loop of a growth factor protein by oxidizing the cysteine PT residues.
XX PS Example 26; Page 49; 102pp; English.
XX The sequence represents a dimeric bicyclic peptide of the invention, CC whose 3-dimensional structure is modelled on the expose loop of human CC VEGF (vascular endothelial growth factor). The invention relates to a CC method of producing a monomeric monocyclic peptide by a measuring beta- CC beta carbon separation distances on opposite antiparallel strands of a CC peptide loop fragment from an exposed loop of a growth factor protein and CC cyclising the peptide by oxidising the cysteine residues. The monocyclic CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic CC peptides) and a cyclic peptide with at least one amino acid deleted prior CC to cyclisation are used to interfere with angiogenesis, CC neovascularisation or lymphangiogenesis in a mammal with a condition CC characterised by angiogenesis, neovascularisation or lymphangiogenesis. CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold CC trauma, substance-induced neovascularisation of the liver, excessive CC hormone-related angiogenic dysfunction, diabetes induced neovascular CC sequelae, hypertension induced neovascular sequelae, or chronic liver CC infection. The peptides are also used to modulate vascular permeability CC in a mammal (the mammal has a condition characterised by fluid CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, CC or brain). The peptides are used to image blood vessels and lymphatic CC vasculature. The monomeric and bicyclic peptides are used to interfere CC with at least one biological activity induced by VEGF, VEGF-C or -D and CC are also used in combination with an anti-inflammatory agent, to treat a CC chronic inflammation, especially rheumatoid arthritis, psoriasis and CC diabetic retinopathy.
XX SQ Sequence 9 AA;
Query Match 90.9%; Score 50; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DR 1 CCNBEISLIC 9
Db 1 CCNBEISLIC 9
RESULT 3
AAU04553
ID AAU04553 standard; peptide; 9 AA.
XX AC AAU04553;
XX DT 26-SEP-2001 (first entry)
DE VEGF based bicyclic dimeric peptide #10.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
XX Key Location/Qualifiers
FR Disulfide-bond 1
/note= "A disulfide bond forms between residue 1 and residue 17 of the sequence appearing as AAU04527, forming a dimeric peptide"
FR Disulfide-bond 2..9
/note= "This bond cyclises the peptide"
XX WO200152875-A1.
PN 18-JAN-2001; 2001WO-US001533.
XX PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
PR 1/note= "A disulfide bond forms between residue 1 and

FT residue 17 of the sequence appearing as AAU04527, forming
 FT a dimeric peptide".
 FT Disulfide-bond 2..9
 FT /note= "This bond cyclises the peptide"
 XX WO200152875-A1.
 PN 26-JUL-2001.
 XX
 XX PP 18-JAN-2001; 2001WO-US001533.
 XX PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI DR; 2001-442248/47.
 XX
 XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX PS Example 26; Page 49; 102pp; English.
 XX
 CC The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC characterised by angiogenesis, neovascularisation in a mammal with a condition
 CC characterised by diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monocyclic and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX Sequence 9 AA;
 SQ Score 49; DB 4; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+05;
 Matches 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEESLIC 9

Db 1 CCNEETVIC 9

Query Match 89.1%; Score 49; DB 4; Length 8;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9

Db 1 CNEESLIC 8

XX DE VEGF based monocyclic peptide 2.
 XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequeleae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX OS Synthetic.
 XX FH Key Disulfide-bond 1..8
 FT /note= "This bond cyclises the peptide"
 XX PN WO200152875-A1.
 XX PD 26-JUL-2001.
 XX PF 18-JAN-2001; 2001WO-US001533.
 XX PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides) dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC characterised by angiogenesis, neovascularisation in a mammal with a condition
 CC characterised by diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monocyclic and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX Sequence 8 AA;
 SQ Score 46; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 AAU04525 standard; peptide; 8 AA.
 ID AAU04525
 XX AC AAU04525;
 XX DT 26-SEP-2001 (first entry)

Query Match 83.6%; Score 46; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 AAU04539 standard; peptide; 8 AA.
 XX
 AAU04539;
 AC
 XX
 DT 26-SEP-2001 (first entry)
 XX
 VEGF based monocyclic peptide 17.
 DE
 Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS
 XX
 Synthetic.

Key Location/Qualifiers

FT Disulfide-bond 1..8
 /note= "This bond cyclises the peptide"
 XX
 WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PP 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 PA (LUDWIG) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stackler S, Cendron A;
 XX
 DR 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFR (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monomeric
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC characterised by angiogenesis, neovascularisation in a mammal with a condition
 CC characterised by diabetic retinopathy, psoriasis, arthropathy,
 CC hemangiomma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

RESULT 6
 AAU04541
 ID AAU04541 standard; peptide; 8 AA.
 XX
 AAU04541;
 AC
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 19.
 DE
 Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS
 XX
 Synthetic.

Key Location/Qualifiers

FH Disulfide-bond 1..8
 /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PP 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 PA (LUDWIG) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stackler S, Cendron A;
 XX
 DR 2001-442248/47.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFR (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monomeric peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangiomma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Example 25; Page 47; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFR (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monomeric peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangiomma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

CC in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

XX Sequence 8 AA;

Query Match	76.4‡;	Score 42;	DB 4;	Length 8;
Best Local Similarity	75.0‡;	Prd. No.	1.4e+06;	
Matches	2;	Mismatches	0;	Indels 0;
Gaps	0;			

Qy 2 CNEESLIC 9
Db 1 CNEESVYC 8

RESULT 7

AAU04538

standard; peptide: 8 AA.

XX

AC AAU04538;

XX

26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 16.

XX

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequeleae; rheumatoid arthritis;

KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key

FT Disulfide-bond 1..8

/note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176233P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG,

XX DR Hughes RA,

XX STacker S,

XX Cendron A;

XX DR WPI; 2001-442248/47.

XX XX

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176233P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG,

XX DR Hughes RA,

XX STacker S,

XX Cendron A;

XX DR WPI; 2001-442248/47.

XX XX

XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,

CC whose 3-dimensional structure is modelled on the expose loop of human

CC VEGF (vascular endothelial growth factor). The invention relates to a

CC method of producing a monomeric monocyclic peptide by a measuring beca-

CC use carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and

CC cyclising the peptide by oxidising the cysteine residues. The monomeric

CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic

CC peptides) and a cyclic peptide with at least one amino acid deleted prior

CC to cyclisation are used to interfere with angiogenesis,

CC neovascularisation or lymphangiogenesis in a mammal with a condition

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy,

CC hemangioma, vascularised malignant or benign tumour, post-recovery

CC cerebrovascular accident, post angioplasty restenosis, head, heat or cold

CC trauma, substance induced neovascularisation of the liver, excessive

CC hormone-related angiogenic dysfunction, diabetes induced neovascular

CC sequelae, hypertension induced neovascular sequelae, or chronic liver

CC infection. The peptides are also used to modulate muscular permeability

CC in a mammal (the mammal has a condition characterised by fluid

CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

CC or brain. The peptides are used to image blood vessels and lymphatic

CC vasculature. The monomeric and bicyclic peptides are used to interfere

CC with at least one biological activity induced by VEGF, VEGF-C or -D and

CC are also used in combination with an anti-inflammatory agent, to treat a

CC chronic inflammation, especially rheumatoid arthritis, psoriasis and

CC diabetic retinopathy

XX SQ Sequence 8 AA;

Query Match 74.5‡; Score 41; DB 4; Length 8;
Best Local Similarity 75.0‡; Pred. No. 1.4e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
Db 1 CNEESVYC 8

RESULT 6

AAU04540

standard; peptide: 8 AA.

XX ID AAU04540

AC AAU04540;

XX DT 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 18.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequeleae; rheumatoid arthritis;

KW KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key

FT Disulfide-bond 1..8

/note= "This bond cyclises the peptide"

XX PN WO200152875-A1.

XX PN WO200152875-A1.

XX PD 26-JUL-2001.

XX PR 26-JUL-2001.

XX PR 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176233P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG,

XX DR Hughes RA,

XX STacker S,

XX Cendron A;

XX DR WPI; 2001-442248/47.

XX XX

XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,

CC whose 3-dimensional structure is modelled on the expose loop of human

CC VEGF (vascular endothelial growth factor). The invention relates to a

CC method of producing a monomeric monocyclic peptide by a measuring beca-

CC use carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and

CC cyclising the peptide by oxidising the cysteine residues. The monomeric

CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic

CC peptides) and a cyclic peptide with at least one amino acid deleted prior

CC to cyclisation are used to interfere with angiogenesis,

CC

The sequence represents a monomeric monocyclic peptide of the invention,

CC whose 3-dimensional structure is modelled on the expose loop of human

CC VEGF (vascular endothelial growth factor). The invention relates to a

CC method of producing a monomeric monocyclic peptide by cyclizing a peptide loop fragment

CC from an exposed loop of a growth factor protein by oxidizing the cysteine

CC residues.

XX Example 25; Page 47; 102pp; English.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,

whose 3-dimensional structure is modelled on the expose loop of human VEGRD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, vasculitis, haemangoma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularization of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular disease, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C, or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 8 AA;

Query Match	Score	DB	Length
Best Local Similarity	70.9%	4	8;
Matches	Pred. No. 1.4e+06;		
QY	2 CNEEBLIC 9		
Db	1 CNEDSFIC 8		

Sequence 8 AA;

Query Match	Score	DB	Length
Best Local Similarity	70.9%	4	8;
Matches	Pred. No. 1.4e+06;		
QY	2 CNEEBLIC 9		
Db	1 CNEDSFIC 8		

Sequence 8 AA;

Query Match	Score	DB	Length
Best Local Similarity	75.0%	4	8;
Matches	Pred. No. 1.4e+06;		
QY	2 CNEEBLIC 9		
Db	1 CNEDSFIC 8		

RESULT 10

AAU08460

ID AAU08460 standard; Peptide; 8 AA.

AAU08460;

Db AAU08460;

XX AC AC;

XX DT 21-NOV-2001 (first entry)

XX PR 21-NOV-2001 (first entry)

XX PR Peptide C6 encoded by human VEGF-C forward primer C6-F.

XX PR DE

XX PR XX

XX PR Human: vascular endothelial growth factor; VEGF-C; vasculogenesis;

XX PR KW angiogenesis; blood vessel; cancer; proliferative retinopathy; rheumatoid arthritis; cardiovascular; psoriasis;

XX PR KW age-related macular degeneration; rheumatoid arthritis; cardiovascular; primer; mutant; mutein.

XX PR XX Homo sapiens.

XX PR OS Synthetic.

XX PR PN WO200162942-A2.

XX PR XX WO200162942-A2.

XX PR XX 30-AUG-2001.

XX PR XX 26-FEB-2001; 2001WO-US006113.

XX PR PR 25-FEB-2000; 2000US-0105205P.

XX PR XX 18-MAY-2000; 2000US-0205331P.

XX PR PA (LUDWIG INST CANCER RES.

XX PR PA (LICEN) LICENTIA OY.

XX PR PI Alitalo K, Jeltsch MM;

XX PR XX WPI; 2001-535640/59.

XX DR DR N-PSDB; AAS12807.

XX PT PT Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them.

XX PS PS Claim 9; Fig 7C; 261pp; English.

XX CC The present invention relates to polypeptides that bind cellular

CC Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them.

XX Claim 9; Fig 7C; 261pp; English.

CC The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the CC polynucleotides encoding them, and their use for identifying agents that CC modulate interactions between VEGFs and their receptors. VEGFs and their CC receptors play an important role in vasculogenesis, the development of CC the embryonic vasculature from early differentiating endothelial cells CC and angiogenesis, the process of forming new blood vessels from pre-existing ones. Modulators of interactions between VEGF and its receptors CC may be used to treat dysfunction of the endothelial cell regulatory CC system. Such disorders include cancers, abnormal angiogenesis, CC proliferative retinopathies, age-related macular degeneration, rheumatoid CC arthritis and psoriasis. The polypeptides of the invention exhibit unique CC receptor binding profiles compared to known naturally occurring VEGFs. CC AAU08446 AAU08454 represent the Peptides A1-A9 which are encoded by human CC VEGF-A forward primers used in the methods of the present invention

XX Sequence 8 AA;

Query Match

Best Local Similarity

Matches

QY

5; Conservative

Db

5; Mismatches

XX

PT PT Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them.

XX Claim 9; Fig 7C; 261pp; English.

CC The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the CC polynucleotides encoding them, and their use for identifying agents that CC modulate interactions between VEGFs and their receptors. VEGFs and their CC receptors play an important role in vasculogenesis, the development of CC the embryonic vasculature from early differentiating endothelial cells CC and angiogenesis, the process of forming new blood vessels from pre-existing ones. Modulators of interactions between VEGF and its receptors CC may be used to treat dysfunction of the endothelial cell regulatory CC system. Such disorders include cancers, abnormal angiogenesis, CC proliferative retinopathies, age-related macular degeneration, rheumatoid CC arthritis and psoriasis. The polypeptides of the invention exhibit unique CC receptor binding profiles compared to known naturally occurring VEGFs. CC AAU08446 AAU08454 represent the Peptides A1-A9 which are encoded by human CC VEGF-A forward primers used in the methods of the present invention

XX Sequence 8 AA;

Query Match

Best Local Similarity

Matches

QY

5; Conservative

Db

5; Mismatches

XX

receptors for vascular endothelial growth factors (VEGFS), the polynucleotides encoding them, and their use for identifying agents that modulate interactions between VEGFs and their receptors. VEGFs and their receptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from pre-existing ones. Modulators of interactions between VEGF and its receptors may be used to treat dysfunction of the endothelial cell regulatory system. Such disorders include cancers, abnormal angiogenesis, proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique receptor binding profiles compared to known naturally occurring VEGFs. AAU08455-AAU08463 represent the peptides C1-C9 which are encoded by human VEGF-C forward primers used in the methods of the present invention.

Sequence 8 AA;

Query Match	60.0%	Score 33;	DB 4;	Length 8;
Best Local Similarity	71.4%	Pred. No. 1.4e+06;		
Matches	5;	Conservative	2;	Indels 0;
Qy	1 CCNEESL 7			
Db	2 CCNSEGL 8			

RESULT 11
ABR29619

ID	ABR29619	standard; Peptide; 9 AA.
XX		
AC	ABR29619;	
XX		
DT	19-MAY-2003	(first entry)

XX		
DE	Human cancer-related protein 192P2G7 HLA peptide #1263.	
XX		
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;	
KW	human leukocyte antigen.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200283921-A2.	

24-OCT-2002.

XX		
DR	Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;	
XX		
PI	Morrison K, Morrison RK, Raitano AB;	
XX		
PP	WPI; 2003-075555/07.	

XX		
PR	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	
XX		
PA	(AGEN-) AGENSYS INC.	
XX		
PD	Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;	
XX		
PP	10-APR-2002; 2002WO-US011654.	

XX		
PR	10-APR-2001; 2001US-0282739P.	
PR	10-APR-2001; 2001US-0283112P.	
PR	25-APR-2001; 2001US-0286630P.	

XX (AGEN-) AGENSYS INC.

24-OCT-2002.

XX		
DR	Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;	
XX		
PI	Morrison K, Morrison RK, Raitano AB;	
XX		
PS	WPI; 2003-075555/07.	

XX		
PT	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	
XX		
PA	Claim 13; Page 431; 1021pp; English.	

XX		
PI	The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ7168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response.	
XX		
CC	The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and	

CC		
CC	Cancer patients. The proteins and peptides are useful as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

CC		
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention

Sequence 9 AA;

Query Match	60.0%	Score 33;	DB 6;	Length 9;
Best Local Similarity	71.4%	Pred. No. 1.4e+06;		
Matches	5;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;
Qy	1 CCNEESL 7			
Db	1 CCNAEAL 7			

RESULT 12
ABR28797

ID	ABR28797	standard; peptide; 9 AA.
XX		
AC	ABR28797;	
XX		
DT	19-MAY-2003	(first entry)

XX		
DE	Human cancer-related protein 192P2G7 HLA peptide #241.	
XX		
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;	
KW	human leukocyte antigen.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200283921-A2.	

24-OCT-2002.

XX		
DR	WPI; 2003-075555/07.	
XX		
PS	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	
XX		
PT	The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ7168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response.	

CC		
CC	The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and	

CC		
CC	cancer patients. The proteins and peptides are useful as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	as therapeutic agents. The proteins and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example	

Sequence 9 AA;

QY 1 CCNEESL 7
Db 1 CCNAEAL 7

RESULT 1.3
ID ABR29456
XX ABR29456 standard; peptide; 9 AA.
AC ABR29456;
XX DT 19-MAY-2003 (first entry)
XX Human cancer-related protein 192P2G7 HLA peptide #258.

DE Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
OS WO200283921-A2.
XX PD 24-OCT-2002.
XX XX 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
cancer patients.
XX PS Claim 13; Page 419; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX SQ Sequence 9 AA;

Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCNEESL 7
Db 1 CCNAEAL 7

RESULT 1.5
ID ABR29789
XX ABR29789 standard; peptide; 9 AA.
AC ABR29789;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 192P2G7 HLA peptide #1233.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX OS Homo sapiens.

RESULT 14
ABR28814
ID ABR28814 standard; peptide; 9 AA.
XX

XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYN INC.
 XX
 PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 431; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

SQ Sequence 9 AA;

Query Match 60.0%; Score 33; DB 6; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCNEESL 7
 Db 3 CCNAEAL 9

Search completed: September 5, 2004, 11:03:33
 Job time : 38.3333 secs

This Page Blank (uspto)


```

; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-33

Query Match          90.9%; Score 50; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-761-636A-20
; Sequence 20, Application US/09761636A
; Patent No. US2002005218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-20

Query Match          78.2%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US2002005218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-22

Query Match          89.1%; Score 49; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

```

```

; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-22

Query Match 76.4%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-761-636A-19
; SEQ ID NO: 19
; Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 106448505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-19

Query Match 74.5%; Score 41; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-761-636A-19
; SEQ ID NO: 19
; Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 106448505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-19

Query Match 70.9%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
US-09-761-636A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 133
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Peptide
US-09-761-636A-133

Query Match 63.6%; Score 35; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
US-09-761-636A-142
; Sequence 142, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 142
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Peptide
US-09-761-636A-142

```

OTHER INFORMATION: peptide
US-09-795-006A-142

Query Match Score 33; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCNEESL 7
Db 2 CCNSEGGL 8

RESULT 11
US-10-436-549-605

; Sequence 605, Application US/10436549
; Publication No. US20040038307A1

; GENERAL INFORMATION
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Dr. Xun
; APPLICANT: Chan, John W.
; APPLICANT: Zhang, Shengsheng
; APPLICANT: Benkovic, Stephen J.

; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN PROTEIN ANALYSIS

; FILE REFERENCE: ENG-EPO-001

; CURRENT APPLICATION NUMBER: US/10/436-549

; CURRENT FILING DATE: 2003-05-12

; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,223

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/430,948

; PRIOR FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 60/433,319

; PRIOR FILING DATE: 2002-12-13

; PRIOR APPLICATION NUMBER: 60/393,137

; PRIOR FILING DATE: 2002-07-01

; NUMBER OF SEQ ID NOS: 614

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 605

; LENGTH: 5

; TYPE: PRT
; ORGANISM: human

US-10-436-549-605

Query Match Score 29; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNE 4
Db 2 CCNE 5

RESULT 12
US-10-072-602B-292

; Sequence 292, Application US/10072602B
; Publication No. US20030109670A1

; GENERAL INFORMATION
; APPLICANT: Cognex, Inc.
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Louedes J.
; APPLICANT: Grille, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 292
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Conus dalli
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1) .(9)
; OTHER INFORMATION: Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is Tyr,
; Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Ile,
; OTHER INFORMATION: 121-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
; OTHER INFORMATION: O-Phospho-Tyr
US-10-072-602B-292

Query Match Score 27; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCNEESLIC 9
Db 1 CCXXXKLCC 9

RESULT 13
US-09-984-271-199

; Sequence 199, Application US/09984271
; Publication No. US20030040088A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030PL
; CURRENT APPLICATION NUMBER: US/09/984,271
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 199
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-984-271-199

Query Match Score 26; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNE 4
Db 1 CCNQ 4

<pre> RESULT 14 US-09-984-276-199 ; Sequence 199, Application US/0984276 ; Publication No. US20030017500A1 ; GENERAL INFORMATION: ; APPLICANT: Rosen et al. ; TITLE OF INVENTION: 71 Human Secreted Proteins ; FILE REFERENCE: P2030P1 ; CURRENT APPLICATION NUMBER: US/09/984-276 ; CURRENT FILING DATE: 2001-10-29 ; PRIOR APPLICATION NUMBER: 09/482,273 ; PRIOR FILING DATE: 2000-01-13 ; PRIOR APPLICATION NUMBER: 60/092,921 ; PRIOR FILING DATE: 1998-07-15 ; PRIOR APPLICATION NUMBER: 60/092,922 ; PRIOR FILING DATE: 1998-07-15 ; PRIOR APPLICATION NUMBER: 60/092,956 ; PRIOR FILING DATE: 1998-07-15 ; NUMBER OF SEQ ID NOS: 267 ; SEQ ID NO: 199 ; LENGTH: 8 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-984-276-199 </pre>	<pre> Search completed: September 5, 2004, 11:15:59 Job time : 36.6667 secs Db : : 1 CCHEQ 5 </pre>
---	--

<pre> Query Match 47.3%; Score 26; DB 12; Length 8; Best Local Similarity 75.0%; Pred. No. 1.2e+06; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0; </pre>	<pre> Qy 1 CCNB 4 Db 1 CCNQ 4 </pre>
--	--

<pre> RESULT 15 US-10-149-138-2497 ; Sequence 2497, Application US/10149138 ; Publication No. US20040018971A1 ; GENERAL INFORMATION: ; APPLICANT: Fikes, John ; APPLICANT: Sette, Alessandro ; APPLICANT: Sidney, John ; APPLICANT: Southwood, Scott ; APPLICANT: Chesnut, Robert ; APPLICANT: Cells, Esteban ; APPLICANT: Keogh, Elissa ; TITLE OF INVENTION: Inducing Cellular Immune Responses to ; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions ; FILE REFERENCE: 2060_0140001 ; CURRENT APPLICATION NUMBER: US/10/149,138 ; CURRENT FILING DATE: 2002-06-10 ; PRIOR APPLICATION NUMBER: PCT/US00/33591 ; PRIOR FILING DATE: 2000-12-11 ; PRIOR APPLICATION NUMBER: US 09/458,299 ; NUMBER OF SEQ ID NOS: 4641 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 2497 ; LENGTH: 8 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: OTHER INFORMATION: Artificially Synthesized Peptide US-10-149-138-2497 </pre>	<pre> Qy 1 CCNEE 5 </pre>
--	------------------------------

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 11:01:38 ; Search time 12 Seconds
 38.719 Million cell updates/sec
 (without alignments)

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62

Gapp 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/pctodata/2/iaa/5A-COMB.pep:*

2: /cgn2_6/pctodata/2/iaa/5B-COMB.pep:*

3: /cgn2_6/pctodata/2/iaa/6A-COMB.pep:*

4: /cgn2_6/pctodata/2/iaa/6B-COMB.pep:*

5: /cgn2_6/pctodata/2/iaa/PCTUS-COMB.pep:*

6: /cgn2_6/pctodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	30	54.5	8	3	US-09-100-409A-27	Sequence 27, Appl
2	27	49.1	8	5	PCT-US93-05325-2	Sequence 2, Appl
3	27	49.1	8	5	PCT-US93-05325-30	Sequence 30, Appl
4	27	49.1	8	5	PCT-US93-05325-31	Sequence 31, Appl
5	27	49.1	8	5	PCT-US93-05325-32	Sequence 32, Appl
6	26	47.3	8	4	US-09-089-878-3	Sequence 3, Appl
7	26	47.3	8	4	US-09-482-273-199	Sequence 199, Appl
8	26	47.3	9	3	US-09-258-754-113	Sequence 13, Appl
9	26	47.3	9	3	US-09-139-802-93	Sequence 93, Appl
10	26	47.3	9	3	US-09-042-107-13	Sequence 107, Appl
11	26	47.3	9	4	US-09-059-786-93	Sequence 93, Appl
12	26	47.3	9	4	US-08-926-914-93	Sequence 93, Appl
13	26	47.3	9	4	US-09-723-250D-13	Sequence 13, Appl
14	25	45.5	8	1	US-08-107-411-7	Sequence 7, Appl
15	25	45.5	8	1	US-08-397-632A-100	Sequence 100, Appl
16	25	45.5	8	3	US-09-258-754-49	Sequence 49, Appl
17	25	45.5	8	3	US-09-042-107-49	Sequence 49, Appl
18	25	45.5	8	4	US-09-722-250D-49	Sequence 49, Appl
19	25	45.5	9	4	US-09-535-852-1205	Sequence 1205, Appl
20	24	43.6	4	3	US-08-750-142B-17	Sequence 17, Appl
21	24	43.6	5	4	US-09-708-606-22	Sequence 22, Appl
22	24	43.6	6	4	US-09-708-606-8	Sequence 8, Appl
23	24	43.6	6	4	US-09-708-606-26	Sequence 26, Appl
24	24	43.6	7	3	US-08-150-142B-37	Sequence 37, Appl
25	24	43.6	7	4	US-09-717-364A-32	Sequence 32, Appl
26	24	43.6	7	4	US-09-708-606-11	Sequence 11, Appl
27	24	43.6	8	4	US-09-187-859-917	Sequence 917, Appl

ALIGNMENTS

RESULT 1
 US-09-100-409A-27
 ; Sequence 27, Application US/09100409A
 ; Patent No. 6090388

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR PREVENTION AND TREATMENT OF HIV INFECTION AND IMMUNE DISORDERS

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESS: MORGAN & FINNEGANS

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version 1.25

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100, 409A

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME:

; REGISTRATION NUMBER: 1151-4154

; REFERENCE/DOCKET NUMBER: 1151-4154

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-8800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO. 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

US-09-100-409A-27

Query Match Score 30; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 3e+05;
 Matches 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
 |||:
 1 CNQG3FLC 8

Ds

RESULT 2
PCT-US93-05325-2
Sequence 2, Application PC/TU9305325
GENERAL INFORMATION:
APPLICANT: SRI, INTERNATIONAL
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
ADDRESS: COUNSEL
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05325
FILING DATE: 19930603
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/894,497
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: PCT-2679
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 859-2446
TELEFAX: (415) 859-3880
TELEX: 334486
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 3
OTHER INFORMATION: /note= "This position is modified
OTHER INFORMATION: With Acm."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is modified
OTHER INFORMATION: With Acm."
PCT-US93-05325-30

Query Match 49.1%; Score 27; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCNNEES 6
Db 3 CCNTSS 8

RESULT 4
PCT-US93-05325-31
Sequence 31, Application PC/TU9305325
GENERAL INFORMATION:
APPLICANT: SRI, INTERNATIONAL
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
ADDRESS: COUNSEL
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05325
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:

RESULT 3
PCT-US93-05325-30
Sequence 30, Application PC/TU9305325
GENERAL INFORMATION:
APPLICANT: SRI, INTERNATIONAL
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
ADDRESS: COUNSEL
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

NAME: CLARK, JANET P. 34,799
 REGISTRATION NUMBER: 34,799
 REFERENCE DOCKET NUMBER: PCT-2679
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 859-2446
 TELEX: (415) 859-3880
 SEQUENCE FOR SEQ ID NO: 31:
 LENGTH: 8 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: both
 MOLECULE TYPE: peptide
 PCT-US93-05325-31

RESULT 5
 Query Match 49.1%; Score 27; DB 5; Length 8;
 Best Local Similarity 66.7%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEEES 6
 Db 3 CCNTSS 8

RESULT 6
 US-09-089-878-3
 ; Sequence 3, Application US/09089878
 ; GENERAL INFORMATION:
 ; PATENT NO. 648528
 ; APPLICANT: Groat, Randall G.
 ; APPLICANT: O' Connor, Thomas P.
 ; APPLICANT: Mermel, Brion
 ; TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
 ; FILE PREFERENCE: 00098/111001
 ; CURRENT APPLICATION NUMBER: US/09/089,878
 ; EARLIER APPLICATION NUMBER: US 60/085,615
 ; EARLIER FILING DATE: 1998-06-03
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Feline immunodeficiency virus
 US-09-089-878-3

Query Match 47.3%; Score 26; DB 4; Length 8;
 Best Local Similarity 37.5%; Pred. No. 3e+05; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CNEESJC 9
 Db 1 CNQNQFFC 8

RESULT 7
 US-09-482-273-199
 ; Sequence 199, Application US/09482273
 ; GENERAL INFORMATION:
 ; PATENT NO. 6534631
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: F2030P1
 ; CURRENT APPLICATION NUMBER: US/09/482,273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,922
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,956
 ; EARLIER FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 267
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 199
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-482-273-199

Query Match 47.3%; Score 26; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 3e+05; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCNE 4

NAME/KEY: Disulfide-bond
 LOCATION: 3..4
 OTHER INFORMATION: /note= "This position has disulfide bond to corresponding position of identical sequence."
 PCT-US93-05325-32

|||:
Db 1 CCNQ 4

RESULT 8
US-09-258-754-13
; Sequence 13, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LJ 3442
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: US/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-13

Qy 1 CCNQ 4
Db 1 CCNQ 4

RESULT 10
US-09-042-107-13
; Sequence 13, Application US/09042107
; Patent No. 623287
; GENERAL INFORMATION
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-13

Qy 1 CCNQ 4
Db 1 CCNQ 4

RESULT 11
US-09-659-786-93
; Sequence 93, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; Molecules That Home to Angiogenic Vasculature Using
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; SEQ ID NO 93
; PRIORITY NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIORITY NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-659-786-93

Qy 1 CCNQ 4
Db 1 CCNQ 4

RESULT 12
US-08-926-914-93
; Sequence 93, Application US/08926914

Patent No. 6576239
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LJ 2725
REFERENCE/DOCKET NUMBER: P-LJ 2725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-926-914-93

Query Match Score 47.3%; Pred. No. 3e+05; Length 9;
Best Local Similarity 44.4%; Matches 4; Indels 0; Gaps 0;

Query 1 CCNEESLIC 9
Db 1 CPEHRSLVC 9

RESULT 13
US-09-722-250D-13
Sequence 13, Application US/09722250D
Patent No. 6610651
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or Tissues
FILE REFERENCE: P-LJ 4514
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US/09/722,250D
NUMBER OF SEQ ID NOS: 437
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 13
LENGTH: 9
TYPE: PRT
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Query Match Score 47.3%; Pred. No. 3e+05; Length 9;
Best Local Similarity 33.3%; Matches 2; Indels 0; Gaps 0;

Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CONNEESLIC 9
Db 1 CLAKENVYC 9

RESULT 14
US-08-107-411-7
Sequence 7, Application US/08107411
Patent No. 5340726
GENERAL INFORMATION:
APPLICANT: Waxman, Lloyd
APPLICANT: Connolly, Thomas M.
APPLICANT: Keller, Paul
TITLE OF INVENTION: PROTEIN FOR INHIBITING COLLAGEN-STIMULATED PLATELET AGGREGATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: N.J.
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,411
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/844,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parr, Richard S.
REGISTRATION NUMBER: 32,586
REFERENCE/DOCKET NUMBER: 18415
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
TELEFAX: (908) 594-4720
TELEX: () 138825
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDBEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-107-411-7

Query Match Score 45.5%; Pred. No. 3e+05; Length 8;
Best Local Similarity 60.0%; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCNNEE 5
Db 4 CCDEK 8

RESULT 15
US-08-397-633A-100
Sequence 100, Application US/08397633A
Patent No. 5773577
GENERAL INFORMATION:
APPLICANT: Capello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: FLIEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-2449
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-633A-100

Query Match 45.5%; Score 25; DB 1; Length 8;
Best Local Similarity 3.5%; Pred. No. 3e+05;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 CNESSLIC 9
| : : |
DB 1 CGQSKVIC 8

Search completed: September 5, 2004, 11:07:04
Job time : 12 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 11:00:28 ; Search time 11.6667 Seconds
74.205 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLITSVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pir1;*

2: pir2;*

3: pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	1.7	34.0	8	G33098	205K exoantigen - 118K stomach cancer antigen - human (fragment)
2	1.6	32.0	9	A60356	118K stomach cancer antigen - human (fragment)
3	1.6	32.0	9	P10247	19 heavy chain CRD
4	1.5	30.0	5	A50521	glycogen phosphorylase
5	1.5	30.0	6	165545	MHC H2-L antigen -
6	1.5	30.0	7	P0932	T-cell receptor beta
7	1.5	30.0	8	P0803	T-cell receptor alpha
8	1.4	28.0	5	B60274	major protein anti-T-cell receptor ga
9	1.4	28.0	6	A61946	fibroblast growth
10	1.4	28.0	8	A42057	neutral protease
11	1.4	28.0	8	A35180	sperm-activating protein
12	1.4	28.0	9	A60522	orf downstream to b
13	1.4	28.0	9	B41983	seminal vesicle protein
14	1.4	28.0	9	152974	laminin B1 - waste
15	1.3	26.0	6	A19421	Na+/K+-exchanging
16	1.3	26.0	6	S29881	formylglycinamide
17	1.3	26.0	7	A12016	aggregan - bovine
18	1.3	26.0	7	S42620	metallothionein is
19	1.3	26.0	8	S56220	unidentified 6.5/3
20	1.3	26.0	8	P00701	Ig heavy chain CRD
21	1.3	26.0	6	P10268	hypothetical collagen
22	1.2	24.0	6	A5039	seed protein ws-5
23	1.2	24.0	7	B61491	alcohol dehydrogenase
24	1.2	24.0	8	S71919	enolase f - bovin
25	1.2	24.0	8	S10783	coat protein beta
26	1.2	24.0	9	S13636	kidney and bladder
27	1.2	24.0	9	G38502	endosperm protein,
28	1.2	24.0	9	S70334	tyrosine-melanocyt
29	1.1	22.0	4	A32039	PT0247

schwannomin - mouse

R phycoerythrin al

DNA protein - Pse

Ig heavy chain CRD

catch-relaxing PeP

chidrofolate redu

DNA topoisomerase

Ig H chain V-D-J r

acylase - Kluyvera

endoglycosidases

nitrated reductase

Lectin - potato (f

T-cell receptor be

gene Cftr protein

major postsynaptic

granulocyte-colony

alignments

RESULT 1

G33098

205K exoantigen - malaria parasite (*Plasmodium falciparum*) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C;Accession: G33098

R;Nichols, J.H.; Hader, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: G33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <NIC>

Query Match 34.0%; Score 17; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPPLTSV 8

Db 2 VPXLV 7

RESULT 2

A60356

118K stomach cancer antigen - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999

C;Accession: A60356

R;Shiraishi, Y.

Int. J. Cancer 45, 783-787, 1990

A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens from

A;Reference number: A60356; PMID:30216080; PMID:2323853

A;Accession: A60356

A;Molecule type: protein

A;Residues: 1-9 <SH1>

C;Keywords: glycoprotein

Query Match 32.0%; Score 16; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPPLTSV 8

Db 1 IPLKEY 6

RESULT 3

PT0247

Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0247
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J;Exp. Med.;173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
 A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0247
 A;Molecule type: DNA
 A;Residues: 1-9 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 32.0%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SVPLTS 7
 Db 2 SAPIDS 7

RESULT 4
 A60521 Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
 N;Alternate names: Glycogen phosphorylase b
 C;Species: Liza ramada
 C;Accession: A60521
 R;Bonanotte, L.; Bonanotte, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
 A;Reference number: A60521; MUID:90227907; PMID:2103669

A;Accession: A60521
 A;Molecule type: protein
 A;Residues: 1-5 <BON>
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 P;Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment
 Query Match 30.0%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVP 4
 Db 3 SVP 5

RESULT 5
 I65546 MHC H2-L antigen - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: I65546
 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
 Cell 44, 261-272, 1986
 A;Title: Detailed analysis of the mouse H-2K^b promoter: Enhancer-like sequences and thei
 A;Reference number: I52778; MUID:86106202; PMID:3510743
 A;Accession: I65546
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <REBS>
 A;Cross-references: GB:M12483; PIDN:AAA39663.1; PID:g554234

Query Match 30.0%; Score 15; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VPLT 6
 Db 2 VPCT 5

RESULT 6

PH0932 T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0932
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A;Reference number: PH0891; MUID:92078857; PMID:1896012
 A;Accession: PH0891
 A;Residues: 1-7 <GOL>
 A;Experimental source: complete Freund's adjuvant-immunized lymph node
 A;Molecule type: mRNA
 A;Residues: 1-7 <GOL>
 A;Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSVPL 4
 Db 1 CASP 4

RESULT 7
 PH0803 T-cell receptor alpha chain (J2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PH0803
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078846; PMID:1896010
 A;Accession: PH0803
 A;Molecule type: mRNA
 A;Residues: 1-8 <CAS>
 A;Cross-references: EMBL:X60912
 A;Experimental source: T lymphocyte

Query Match 30.0%; Score 15; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSVPLT 6
 Db 1 CAAGIT 6

RESULT 8
 E60274 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
 C;Species: Mycobacterium tuberculosis
 C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: E60274
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A;Title: Isolation and partial characterization of major protein antigens in the culture
 A;Reference number: A60274; MUID:9109989; PMID:1898899
 A;Accession: E60274
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <NRG>

Query Match 28.0%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLT 6
 Db 3 PIT 5

RESULT 6

RESULT 9		Qy	4 PLTS 7				
F41946		Db	1 PLIS 4				
T-cell receptor gamma chain (1a.27) - mouse (fragment)							
C;Species: Mus musculus (house mouse)							
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999							
R;Whetstall, M.; Mosley, R.L.; Whetstall, L.; Schaeffer, F.V.; Miller, K.S.; Klein, J.R.							
Mol. Cell. Biol. 11, 5902-5909, 1991							
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge							
A;Reference number: A41946; PMID:92049316; PMID:1658619							
A;Accession: F41946							
A;Status: preliminary; not compared with conceptual translation							
A;Molecule type: DNA							
A;Residues: 1-6 <WHE>							
C;Keywords: T-cell receptor							
RESULT 10		Qy	28.0% Score 14; DB 2; Length 6;				
A42057		Db	0; Gaps 0; Indels 0;				
fibroblast growth factor receptor 1, secreted - mouse (fragment)							
C;Species: Mus musculus (house mouse)							
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999							
C;Accession: A2057							
R;Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.							
Mol. Cell. Biol. 12, 82-88, 1992							
A;Title: Differential splicing in the extracellular region of fibroblast growth factor 1							
A;Reference number: A42057; PMID:92107200; PMID:1309595							
A;Accession: A42057							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-8 <WER>							
A;Cross-references: GB:M80363							
C;Keywords: growth factor receptor							
RESULT 11		Qy	28.0% Score 14; DB 2; Length 8;				
A35180		Db	0; Gaps 0; Indels 0;				
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)							
C;Species: Rattus norvegicus (Norway rat)							
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996							
C;Accession: A35180							
R;Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.							
J. Biol. Chem. 265, 5809-5815, 1990							
A;Title: Purification of a novel type of calcium-activated neutral protease from rat bra							
A;Reference number: A35180; PMID:90302830; PMID:2318836							
A;Accession: A35180							
A;Status: preliminary							
A;Molecule type: protein							
A;Residues: 1-8 <YOS>							
C;Keywords: hydrolase							
RESULT 12		Qy	28.0% Score 14; DB 2; Length 8;				
A40522		Db	0; Gaps 0; Indels 0;				
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)							
C;Species: Diadema setosum							
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000							
C;Accession: A40522							
R;Yoshino, K.I.; Kurita, M.; Nomura, K.; Takao, T.; Shimomishi, Y.; Suzuki							
Comp. Biochem. Physiol. B 95, 423-429, 1990							
A;Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchi							
A;Reference number: A60522; PMID:90227916; PMID:2158412							
A;Accession: A60522							
A;Molecule type: protein							
A;Residues: 1-9 <YOS>							
C;Superfamily: unassigned animal peptides							
F;2-9/Disulfide bonds: #status experimental							
RESULT 13		Qy	28.0% Score 14; DB 2; Length 9;				
B41983		Db	0; Gaps 0; Indels 0;				
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)							
C;Species: Azotobacter vinelandii							
C;Date: 01-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999							
C;Accession: B41983							
R;Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stieffel, E.I.							
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992							
A;Title: Unification of the ferritin family of proteins.							
A;Reference number: A41983; PMID:9196129; PMID:154965							
A;Accession: B41983							
A;Status: Preliminary; not compared with conceptual translation							
A;Molecule type: nucleic acid, protein							
A;Residues: 1-9 <GRD>							
A;Cross-references: GB:M83692; NID:9142297; PID:AAA221221; PMID:9142299							
A;Note: Sequence extracted from NCBI Backbone (NBBP:88442)							
RESULT 14		Qy	28.0% Score 14; DB 2; Length 9;				
I52974		Db	0; Gaps 0; Indels 0;				
seminal vesicle protein IV - rat (fragment)							
C;Species: Rattus norvegicus (Norway rat)							
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999							
C;Accession: I52974							
R;Teng, C.T.; Harris, S.E.							
DNA 2, 105-111, 1993							
A;Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites							
A;Reference number: I52974; PMID:83261204; PMID:6307619							
A;Accession: I52974							
A;Status: preliminary; translated from GB/EMBL/DBJ							
A;Molecule type: DNA							
A;Residues: 1-9 <RES>							
A;Cross-references: GB:M27324; NID:g207124; PID:AAA63501.1; PMID:g207125							
C;Genetics:							
A;Gene: SVSIV							

Query Match Score 14; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 LTSV 8
 | | | | ;
 Db 3 LTSL 6

RESULT 15
 I49421
 laminin B1 - western wild mouse (fragment)
 C:Species: Mus spretus (western wild mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I49421
 R:Ro, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
 Mamm Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: I48934; MUID:94319082; PMID:8043949
 A:Accession: I49421
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <RES>
 A:Cross-references: EMBL:U05736; NID:5497073; PIDN:AAB60477.1; PID:g642829

Query Match Score 13; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 SVC 9
 | | | | ;
 Db 3 STC 5

Search completed: September 5, 2004, 11:06:22
 Job time : 11.6667 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1.9	38.0	9	1	MGT_BOVIN	P29177	"Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase."
2	1.4	28.0	8	1	ACT_CARMA	AC	Nucleic Acids Res. 18:17-21 (1990).
3	1.4	28.0	9	1	YBFR_AZQVI	DT	-!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.
4	1.3	26.0	6	1	E101_LITRUM	DT	-!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein (protein)-L-cysteine = DNA (without 6-O-methylguanine) + S-methyl-L-cysteine.
5	1.2	24.0	8	1	AU16_CDPO	DT	-!- SIMILARITY WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
6	1.2	24.0	8	1	FUSS_FUSSO	DR	Intefiro; IPR01497; Methyltransf. 1.
7	1.2	24.0	8	1	UPA1_HUMAN	PROSTRE: PS00374; MGMT; PARTIAL.	
8	1.2	24.0	9	1	FARS_PENMO	KW	DNA repair; Transferase; Methyltransferase.
9	1.2	24.0	9	1	ELA2_TREHY	FT	1 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
10	1.2	24.0	9	1	OXYA_SCYCA	FT	1
11	1.2	24.0	9	1	OXYF_SCYCA	FT	1
12	1.2	24.0	9	1	OXYT_BUFORE	FT	1
13	1.2	24.0	9	1	OXYV_SQUAC	FT	1
14	1.1	22.0	6	1	VP19_HSV1K	FT	1
15	1.1	22.0	7	1	CARP_MYTED	FT	1
16	1.1	22.0	7	1	WNBP1_LBDP	FT	1
17	1.1	22.0	7	1	TPEY_PACDA	FT	1
18	1.1	22.0	8	1	PPK3_PERMAM	FT	1
19	1.1	22.0	9	1	VGLG_HSV2B	FT	1
20	1.1	22.0	9	1	COKE_THROB	FT	1
21	1.1	22.0	9	1	PAR9_ASCSU	FT	1
22	1.1	22.0	9	1	ISOT_CYPCA	FT	1
23	1.1	22.0	9	1	LMP3_LOCMA	FT	1
24	1.1	22.0	9	1	OXYA_SQUAC	FT	1
25	1.1	22.0	9	1	OXYT_ELSFO	FT	1
26	1.1	22.0	9	1	OXYT_OCTVU	FT	1
27	1.1	22.0	9	1	OXYT_RABIT	FT	1
28	1.1	22.0	9	1	PT13_BOVIN	FT	1
29	1.1	22.0	9	1	TAL1_PICJA	FT	1
30	1.1	22.0	9	1	UPA3_HUMAN	AC	P07059; Rel. 34, Created)
31	1.1	22.0	9	1	UPA7_HUMAN	DT	01-OCT-1996 (Rel. 34, Last sequence update)
32	1.0	20.0	7	1	TYE1_LITRUM	DT	01-OCT-1995 (Rel. 38, Last annotation update)
33	1.0	20.0	8	1	UPA8_HUMAN	DT	15-JUL-1999 (Rel. 38, Last annotation update)

ALIGNMENTS							
RESULT 1							
MGMT_BOVIN	STANDARD;	PRT;	9 AA.				
ID	MGMT_BOVIN	STANDARD;	PRT;	9 AA.			
AC	P29177;						
DT	01-DEC-1992	(Rel. 24, Created)					
DT	01-DEC-1992	(Rel. 24, Last sequence update)					
DT	01-OCT-1996	(Rel. 34, Last annotation update)					
DB	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)	(6-O-methylguanine-DNA methyltransferase) (Fragment).					
GN	MGMT						
OS	Bos taurus (Bovine)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi						
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae						
OC	Bovidae; Bovines; Bos.						
RN	[1]						
SEQUENCE.							
RC	TISSUE=Thymus;						
RX	Medline=90174912; PubMed=2308822;						
RA	Rydborg B., Hall J., Karren P.;						
RT	"Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase."						
RL	Nucleic Acids Res. 18:17-21 (1990).						
CC	-!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.						
CC	Iprotein-L-cysteine = DNA (without 6-O-methylguanine) + protein						
CC	S-methyl-L-cysteine.						
CC	WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.						
DR	Intefiro; IPR01497; Methyltransf. 1.						
DR	PROSTRE: PS00374; MGMT; PARTIAL.						
KW	DNA repair; Transferase; Methyltransferase.						
FT	Best Local Similarity	38.0%	Score 19;	DB 1;	Length 9;		
FT	NON_TER	28.6%	Score 1;	DB 1;	Length 9;		
FT	ACT SITE	9	Score 1;	DB 1;	Length 9;		
FT	NON_TER	9	Score 1;	DB 1;	Length 9;		
SEQUENCE	9 AA;	967 MN;	Score 1;	DB 1;	Length 9;		
Qy	3 VPLTSVC 9						
Db	3 IPILTC 9						
RESULT 2							
ID	ACT_CARMA	STANDARD;	PRT;	8 AA.			
AC	P807059;						
DT	01-OCT-1996	(Rel. 34, Created)					
DT	01-OCT-1995	(Rel. 34, Last sequence update)					
DT	15-JUL-1999	(Rel. 38, Last annotation update)					

DE		Best Local Similarity 75.0%; Pred. No. 1.4e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Carcinus maenas (Common shore crab) (Green crab).			
Carcinidae; Malacostraca; Crustacea; Malacostraca;			
Eumalacostraca; Bivalvia; Decapoda; Pleocymemata; Brachyura; Portunoidea; Portunidae; Carcinus.			
NCBI_TAXID=6759;			
[1]			
SEQUENCE.			
Lachaise F., Somme G., Carpenter G., Granjeon B., Webster S., Baghdassarian D.; "A transaldolase. An enzyme implicated in crab steroidogenesis.";			
Endocrine 5:123-32 (1996).			
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.			
-!- SUBCELLULAR LOCATION: Cytoplasmic.			
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 6.8. ITS MW IS: 46 kDa.			
-!- SIMILARITY: Belongs to the actin family.			
InterPro; IPR004000; Actin like.			
PROSITE; PS00406; ACTINS_1; PARTIAL.			
PROSITE; PS00332; ACTINS_2; PARTIAL.			
PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.			
DR DR Structural protein.			
NON_TER 1 1 PROSITE; PS00332; ACTINS_ACT_LIKE; PARTIAL.			
NON_TER 8 8 Sequence 8 AA; 976 MW; 1424005AB22AAE83 CRC64;			
SEQUENCE 8 AA; 976 MW; 1424005AB22AAE83 CRC64;			
Query Match Score 28.0%; DB 1; Length 8;			
Best Local Similarity 40.0%; Pred. No. 1.4e+05; Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
SQ 1 CSVPL 5 2 CVDI 6			
RESSULT 3			
QY NCBI_TAXID=3544; STANDARD; PRT; 9 AA.			
PDB P25825;			
AC 01-MAY-1992 (Rel. 22, Created)			
DT 01-MAY-1992 (Rel. 22, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
RN Hypothetical protein in bfr 3' region (Fragment).			
SEQUENCE FROM N.A. MEDLINE:92196129; PubMed=1549605;			
Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C., Stiebel E.T.; "Unification of the ferritin family of proteins.";			
Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992);			
[1]			
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires an agreement (See http://www.isdb-sib.ch/announce/ or send an email to license@isdb-sib.ch).			
CC ENB1; M3692; AAA2122.1; -			
DR PIR; B41983; B41983.			
KW Hypothetical protein.			
SQ SEQUENCE 9 AA; 947 MW; DF98BSA1B417776D CRC64;			
NON_TER 9 9 Query Match 28.0%; Score 14; DB 1; Length 9;			
RN 0; Gaps 0; Indels 0; Gaps 0;			
SEQUENCE 9 AA; 947 MW; 0B289C45B573767 CRC64;			
RESSULT 4			
QY NCBI_TAXID=104895; STANDARD; PRT; 6 AA.			
PDB P20296;			
AC ID BI01 LITRU			
DT 28-FEB-2003 (Rel. 41, Created)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Electrin 1.			
OS Litoria rubella (Desert tree frog)			
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; NCBI_TAXID=104895;			
RN 0; Gaps 0; Indels 0; Gaps 0;			
SEQUENCE.			
RC TISSUE-Skin secretion;			
RA Wabnitz P.A., Bowie J.H., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog rubellia.";			
RN [1] Peptides from the skin glands of the Australian buzzing tree frog rubellia.";			
RL Aust. J. Chem. 52:639-645(1999).			
-!- SUBCELLULAR LOCATION: Secreted.			
CC -!- TISSUE SPECIFICITY: Skin.			
KW Amphibian defense peptide; Amidation.			
FT MODRES 6 6 AMIDATION.			
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;			
Query Match Score 26.0%; DB 1; Length 6;			
Best Local Similarity 66.7%; Pred. No. 1.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
SQ 1 VPL 5 2 VPI 4			
RESSULT 5			
QY NCBI_TAXID=104895; STANDARD; PRT; 8 AA.			
PDB P2157;			
AC ID AII6 CYDPO			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DE Cydiastatin 6.			
OS Cydia pomonella (Codling moth).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptysia; Tortricoidae; Tortricidae; Olethreutinae; Cydia.			
NCBI_TAXID=82600;			
RN Sequence 6 AA; 792 MW; 0B289C45B573767 CRC64;			
RESSULT 6			
QY NCBI_TAXID=3544; STANDARD; PRT; 8 AA.			
PDB P25825;			
AC 01-MAY-1992 (Rel. 22, Created)			
DT 01-MAY-1992 (Rel. 22, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
RN Hypothetical protein in bfr 3' region (Fragment).			
SEQUENCE FROM N.A. MEDLINE:92196129; PubMed=1549605;			
Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C., Stiebel E.T.; "Unification of the ferritin family of proteins.";			
Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992);			
[1]			
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires an agreement (See http://www.isdb-sib.ch/announce/ or send an email to license@isdb-sib.ch).			
CC ENB1; M3692; AAA2122.1; -			
DR PIR; B41983; B41983.			
KW Hypothetical protein.			
SQ SEQUENCE 9 AA; 947 MW; DF98BSA1B417776D CRC64;			
NON_TER 9 9 Query Match 24.0%; Score 12; DB 1; Length 8;			
RN 0; Gaps 0; Indels 0; Gaps 0;			

Qy	3 VPL 5 :	PRT;	STANDARD;	PRT;	9 AA.
Db	1 LPL 3				
RESULT 6					
FUSS_FUSSO					
ID_FUSSO					
AC_P81070;					
DT_15-JUL-1998 (Rel. 36; Last sequence update)					
DT_15-JUL-1998 (Rel. 36; Last annotation update)					
DT_10-OCT-2003 (Rel. 42; Last annotation update)					
DE_Eusilurus_solani (subsp. <i>Pisi</i>) (Fragment).					
OS_Eusilurus solani (subsp. <i>Pisi</i>) (Neectria haematoxeca)					
OC_Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;					
OC_Hypocreales; Hypocreidae; Nectriaceae; Nectria.					
NCBI_TaxID=70791;					
RN [1]					
RP	STRAIN=ARI 3596; TISSUE=Mycelium;				
RC_Verna J., Gaigal S.V.;					
RA_Verna J., Gaigal S.V.;					
RL_Submitted (JUN-1997) to Swiss-Prot.					
CC_-!- ALLERGEN: Causes an allergic reaction in human.					
KW_Allergen.					
FT_NON_TER 8	Score 12; DB 1; Length 8;				
SQ_SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;	66.7%; Pred. No. 1.4e+05;				
Query Match Score 12; DB 1; Length 8;	Best Local Similarity 66.7%; Pred. No. 1.4e+05;				
Best Local Similarity 66.7%; Pred. No. 1.4e+05;	Matches 1; Mismatches 0; Indels 0; Gaps 0;				
Qy 2 SVP 4	Score 12; DB 1; Length 9;				
Db 6 NVP 8	Best Local Similarity 66.7%; Pred. No. 1.4e+05;				
Matches 1; Mismatches 0; Indels 0; Gaps 0;					
RESULT 7					
UPA1_HUMAN					
ID_UPA1_HUMAN					
AC_P30087;					
DT_01-APR-1993 (Rel. 25; Created)					
DT_01-APR-1993 (Rel. 25; Last sequence update)					
DT_15-MAR-2004 (Rel. 43; Last annotation update)					
DE_Unknown protein from 2D-page of plasma (Spot 2) (Fragment).					
OS_Homo sapiens (Human).					
OC_Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
OC_Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
NCBI_TaxID=9606;					
RN [1]					
RP	SEQUENCE: Plasma;				
RC_MEDLINE=33092937; PubMed=1453097;					
RX_Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,					
RA_Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,					
RA_Hochstrasser D.F.;					
RT_Plasma protein map: an update by microsequencing.";					
RL_Electrophoresis 13.707-714 (1982).					
CC_-!- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 4.9, its MW is: 65 kDa.					
DR_SWISS-2DPAGE; P30087; HUMAN.					
FT_NON_TER 1 1	Score 12; DB 1; Length 8;				
FT_UNSURE 8 8	Best Local Similarity 66.7%; Pred. No. 1.4e+05;				
SQ_SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;	Matches 1; Mismatches 0; Indels 0; Gaps 0;				
Query Match Score 12; DB 1; Length 8;	Best Local Similarity 66.7%; Pred. No. 1.4e+05;				
Best Local Similarity 66.7%; Pred. No. 1.4e+05;	Matches 1; Mismatches 0; Indels 0; Gaps 0;				
Qy 2 SVP 4	Score 12; DB 1; Length 9;				
Db 5 NVP 7	Best Local Similarity 66.7%; Pred. No. 1.4e+05;				
Matches 1; Mismatches 0; Indels 0; Gaps 0;					

FT NON_TER 9 9 RT isolated from the spotted dogfish (*Scyliorhinus caniculus*). ";

SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match Score 12; DB 1; Length 9;
Best Local Similarity 24.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
DB 2 TVP 4

RESULT 10
OXY_SCYCA SCYCA STANDARD; PRT; 9 AA.

ID_OXY_SCYCA AC
ID_P42996; (Rel. 32, Created)
DT_01-NOV-1995 (Rel. 32, Last sequence update)
DT_01-NOV-1995 (Rel. 32, Last annotation update)

DE Asvatocin.
OS Scyliorhinus canicula (Spotted catshark) (Spotted catshark)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Scyliorhinidae;
NCBI_TaxID=7830;

RN [1]
RP SEQUENCE;
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;

RA Chauvet J., Rouillé Y., Chauveau C., Chauvet M.-T., Achter R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasmatocin, two oxytocin-like peptides isolated from the spotted dogfish (*Scyliorhinus caniculus*).";
PROC. NATL. ACAD. SCI. U.S.A. 91:11268-11270(1994).

CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp-horm.

KW Hormone; Amidation. DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
DR P00220; hormone; 1_P-horm.

FT DISULFID 1 6 AMIDATION.

SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match Score 12; DB 1; Length 9;
Best Local Similarity 24.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
DB 6 CPV 8

RESULT 11
OXY_SCYCA SCYCA STANDARD; PRT; 9 AA.

ID_OXY_SCYCA AC
ID_P42997; (Rel. 32, Created)
DT_01-NOV-1995 (Rel. 32, Last sequence update)
DT_01-NOV-1995 (Rel. 32, Last annotation update)

DE Phasmatocin.
OS Scyliorhinus canicula (Spotted catshark) (Spotted catshark)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Scyliorhinidae;
NCBI_TaxID=7830;

RN [1]
RP SEQUENCE;
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;

RA Chauvet J., Rouillé Y., Chauveau C., Chauvet M.-T., Achter R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasmatocin, two oxytocin-like peptides isolated from the spotted dogfish (*Scyliorhinus caniculus*).";
PROC. NATL. ACAD. SCI. U.S.A. 91:11268-11270(1994).

CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp-horm.

KW Hormone; Amidation. DR PROSITE; PS00220; hormone; 1_P-horm.

FT DISULFID 1 6 AMIDATION.

SQ SEQUENCE 9 AA; 983 MW; 17FF476E5A6D04B CRC64;

Query Match Score 12; DB 1; Length 9;
Best Local Similarity 24.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVP 5
DB 5 SCPI 8

RESULT 12
OXY_BUFRÉ BUFRÉ STANDARD; PRT; 9 AA.

ID_OXY_BUFRÉ AC
ID_P42995; (Rel. 32, Created)
DT_01-NOV-1995 (Rel. 32, Last sequence update)
DT_10-OCT-2003 (Rel. 42, Last annotation update)

DE Seritonin (Ser5,Ile8)-oxytocin.

OS Bufuro regularis (Leopard toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; NCBI_TaxID=8390;

RN [1]
RP SEQUENCE;
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=2591488;

RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Achter R.;
RT "A new neurohypophysial peptide, seritonin ((Ser5,Ile8)-oxytocin), identified in a dryness-resistant African toad, *Bufo regularis*.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).

CC -1- FUNCTION: Devoid of oxytocin activity.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp-horm.

KW Hormone; Amidation. DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NBG.

FT DISULFID 1 6 AMIDATION.

SQ SEQUENCE 9 AA; 983 MW; 17FF476E5A6D04B CRC64;

Query Match Score 12; DB 1; Length 9;
Best Local Similarity 24.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVP 5
DB 5 SCPI 8

RESULT 13
OXYV_SQUAC STANDARD; PRT; 9 AA.

ID_OXYV_SQUAC AC
ID_P43000; (Rel. 32, Created)
DT_01-NOV-1995 (Rel. 32, Last sequence update)
DT_01-NOV-1995 (Rel. 32, Last annotation update)

DE Valitocin.

OS Squalus acanthias (Spiny dogfish).
OC Elasmobranchii; Squalidae.
OX Squalus.
RN [1]
RP SEQUENCE;
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;

RA Chauvet J., Rouillé Y., Chauveau C., Chauvet M.-T., Achter R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasmatocin, two oxytocin-like peptides isolated from the spotted dogfish (*Scyliorhinus caniculus*).";
PROC. NATL. ACAD. SCI. U.S.A. 91:11268-11270(1994).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalidae; Squalae; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;

[1]

RN SEQUENCE; PubMed=73031727; PubMed=5083097;
RP MEDLINE=73031727; PubMed=5083097;
RX Achér R., Chauvet J., Chauvet M.-T.;
RA "Phylogeny of the neurohypophysial hormones. Two new active peptides
isolated from a cartilaginous fish, Squalus acanthias.";
RT isolated from a cartilaginous fish, Squalus acanthias.
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]

RP SEQUENCE;
RX MEDLINE=72128038; PubMed=4622083;
RA Achér R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn8-oxytocin) in a selachian fish, the
spiny dog-fish (Squalus acanthias).";
RT C. R. Acad. Sci. (D), Sci. Nat. 274:313-316(1972);
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR Pfam; PF00220; hormone4; 1.-horm.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; 175DD768B456D04B CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSV 3
Db 6 CPV 8

RESULT 14
VP19_HSV1K ID VP19_HSV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38
OS Herpes simplex virus (type 1 / strain KOS).
OC Alphaherpesvirinae; dsDNA viruses, no RNA stage; Herpesviridae;
OC NCBITaxID=10306;
RN SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
expression of UL38, a true late gene involved in capsid assembly.";
RL Virol. 65:769-796 (1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE
EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57646; AAA43830.1;
KW Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 PL 5
Db 5 PL 6

RESULT 15
CARP_MYTED ID CARP_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Bukaoyota Metzoza Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBITaxID=6556;
RN [1]_NCBI_TaxID=6556;
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=33676797;
RA Hirata T., Kubota I., Takabayashi I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
DR PIR; A29342; EC04CR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 673402687669DB0 CRC64;
AMIDATION

Query Match 22.0%; Score 11; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVPL 5
Db 1 AMPM 4

Search completed: September 5, 2004, 11:04:00
Job time : 7 secs

This Page Blank (uspto)